



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: P. D. CHRISTIAN, K. H. J. GORDON and
T. N. HANZLIK

(ii) TITLE OF INVENTION: INSECT VIRUSES AND THEIR USES IN
PROTECTING PLANTS

(iii) NUMBER OF SEQUENCES: 53

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: DORSEY & WHITNEY LLP
- (B) STREET: FOUR EMBARCADERO CENTER, SUITE 3400
- (C) CITY: SAN FRANCISCO
- (D) STATE: CALIFORNIA
- (E) COUNTRY: UNITED STATES OF AMERICA
- (F) ZIP: 94111

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/677,653
- (B) FILING DATE: 3 OCTOBER 2000
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: RICHARD F. TRECARTIN
- (B) REGISTRATION NUMBER: 31,801
- (C) REFERENCE/DOCKET NUMBER: A-58631-4/RFT/NBC

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (415) 781-1989

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATCCACAG NNN

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13

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGGCGATG CCGGCGTCGC GTTCACAG

28

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGGATG CTGGAGTGGC GTCACAG

27

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

C₄ ATGAGCGAGG CCGGCGTCGC GTCACAG

27

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCATCGATGC CGGACTGGTA TCCCAGGGGG

30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCATCGATGC CGGACTGGTA TCCCGAGGGA C

31

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCATCGATGA TCCAGCCTCC TCGCGGCGCC GGATGGGCA

39

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTCTAGATC CATTGCGCAT CCGAAGATGC CCATCCGGC

39

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATCGATTT ATGCCGAGAA GGTAACCAGA GAAACACAC

39

C4 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTCTAGACC AGGTAATATA CCACAACGTG TGTTTCTCT

39

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGGAATT CATTTAGGTG AACTATAGT TCTGCCTCCC CGGAC

45

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGGGGATCC TGGTATCCCA GGGGGGC

27

- (2) INFORMATION FOR SEQ ID NO:13:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGGAAGCTT GTTTTTCTTT CTTTACCA

28

- (2) INFORMATION FOR SEQ ID NO:14:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGGGGATCCG ATGGTATCCC GAGGGACGCT CAGCAGGTGG CATAGG

46

- C₄
(2) INFORMATION FOR SEQ ID NO:15:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAATAATTTT GTTACTTTAG AAGGAGATAT ACATATGAGC GAGCGAGCAC AC

52

- (2) INFORMATION FOR SEQ ID NO:16:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAATAATTTT GTTTAACCTT AAGAAGGAGA TCTACATATG CTGGAGTGGC GTCAC

55

- (2) INFORMATION FOR SEQ ID NO:17:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGAGATCTAC ATATGGGAGA TGCTGGAGTG

30

- (2) INFORMATION FOR SEQ ID NO:18:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAGCGAACG TCGAGAA

17

- (2) INFORMATION FOR SEQ ID NO:19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGGGGATCCT CAGTTGTCAG TGGCGGGGTA G

31

- C4
(2) INFORMATION FOR SEQ ID NO:20:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGGGATCCCT AATTGGCACG AGCGGCGC

28

- (2) INFORMATION FOR SEQ ID NO:21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTACATAT GGCGGCCGCC GTTTCTGCC

29

- (2) INFORMATION FOR SEQ ID NO:22:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AATTACATAT GTTCGCGGCC GCCGTTTCT

29

- (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Phe Ala Ala Ala Val Ser Ala Phe Ala Ala Asn Met Leu Ser Ser Val
1 5 10 15
Leu Lys Ser

- (2) INFORMATION FOR SEQ ID NO:24:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro Thr Leu Val Asp Gln Gly Phe Trp Ile Gly Gly Gln Tyr Ala Leu
1 5 10 15
Thr Pro Thr Ser
 20

- C4
(2) INFORMATION FOR SEQ ID NO:25:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Phe Ala Ala Ala Val Ser
1 5

- (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGCCCCCUG GGAUACCAGG AUC

23

- (2) INFORMATION FOR SEQ ID NO:27:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCAGCAGGTG GCATAGG

17

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCCAT ATG GGC GAT GCC GGC GTC GCG TCA CAG
Met Gly Asp Ala Gly Val Ala Ser Gln
1 5

32

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Gly Asp Ala Gly Val Ala Ser Gln
1 5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCCAT ATG AGC GAG GCC GGC GTC GCG TCA CAG
Met Ser Glu Ala Gly Val Ala Ser Gln
1 5

32

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein - N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Ser Glu Ala Gly Val Ala Ser Gln
1 5

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATG GGA GAT GCT GGA GTG GCG TCA CAG
Met Gly Asp Ala Gly Val Ala Ser Gln
 1 5

27

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Gly Asp Ala Gly Val Ala Ser Gln
 1 5

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGGGATCCC GCGGATTTAT GAGCGAG

27

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGGATCCC GCGGAGACAT GAGCGAGCAC AC

32

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGGGGATCCA GCGACATGAG AGATGCTGGA GTGG

34

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGGGATCCA GCGACATGAG AGATGCTGGA GTGG

34

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGGGGATCCG TTCTGCCTCC CCGGAC

26

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 37..5145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTTCTGCCTC	CCCCGGACGG	TAAATATAGG	GGAACA	ATG	TAC	GCG	AAA	GCG	ACA	54
				Met	Tyr	Ala	Lys	Ala	Thr	
				1				5		
GAC	GTG	GCG	CGT	GTC	TAC	GCC	GCG	GCA	GAT	102
Asp	Val	Ala	Arg	Val	Tyr	Ala	Ala	Ala	Asp	
		10				15			20	
CTG	CAG	CAG	AGA	GCA	GTC	AAG	TTG	GAC	TTC	150
Leu	Gln	Gln	Arg	Ala	Val	Lys	Leu	Asp	Phe	
	25				30				35	
CTA	GAA	ACC	CTC	CAC	AGA	CTG	TAC	TAT	CCG	198
Leu	Glu	Thr	Leu	His	Arg	Gly	Tyr	Tyr	Pro	
	40				45			50		
ACT	TTA	CCC	CCG	ACA	CAA	CAC	CCG	ATC	CTG	246
Thr	Leu	Pro	Pro	Thr	Gln	His	Pro	Ile	Leu	
	55				60			65		
GCA	GAA	GAG	GTT	CTG	CAC	AAT	TTC	GCC	AGG	294
Ala	Glu	Glu	Val	Leu	His	Asn	Phe	Ala	Arg	
			75					80		
									85	

GAG ATA GGG CCG TCT CTG CAC AGC GCA CTT AAG CTA CAT GGG GCA CCG 342
 Glu Ile Gly Pro Ser Leu His Ser Ala Leu Lys Leu His Gly Ala Pro
 90 95 100
 AAC GCC CCC GTC GCA GAC TAT CAC GGG TGC ACC AAG TAC GGC ACC CGC 390
 Asn Ala Pro Val Ala Asp Tyr His Gly Cys Thr Lys Tyr Gly Thr Arg
 105 110 115
 GAC GGC TCG CGA CAC ATT ACG GCC TTA GAG TCT AGA TCC GTC GCC ACA 438
 Asp Gly Ser Arg His Ile Thr Ala Leu Glu Ser Arg Ser Val Ala Thr
 120 125 130
 GGC CGG CCC GAG TTC AAG GCC GAC GCC TCA CTG CTC GCC AAC GGC ATT 486
 Gly Arg Pro Glu Phe Lys Ala Asp Ala Ser Leu Leu Ala Asn Gly Ile
 135 140 145 150
 GCC TCC CGC ACC TTC TGC GTC GAC GGA GTC GGC TCT TGC GCG TTC AAA 534
 Ala Ser Arg Thr Phe Cys Val Asp Gly Val Gly Ser Cys Ala Phe Lys
 155 160 165
 TCG CGC GTT GGA ATT GCC AAT CAC TCC CTC TAT GAC GTG ACC CTA GAG 582
 Ser Arg Val Gly Ile Ala Asn His Ser Leu Tyr Asp Val Thr Leu Glu
 170 175 180
 GAG CTG GCC AAT GCG TTT GAG AAC CAC GGA CTT CAC ATG GTC CGC GCG 630
 Glu Leu Ala Asn Ala Phe Glu Asn His Gly Leu His Met Val Arg Ala
 185 190 195
 TTC ATG CAC ATG CCA GAA GAG CTG CTC TAC ATG GAC AAC GTG GTT AAT 678
 Phe Met His Met Pro Glu Glu Leu Leu Tyr Met Asp Asn Val Val Asn
 200 205 210
 GCC GAG CTC GGC TAC CGC TTC CAC GTT ATT GAA GAG CCT ATG GCT GTG 726
 Ala Glu Leu Gly Tyr Arg Phe His Val Ile Glu Glu Pro Met Ala Val
 215 220 225 230
 AAG GAC TGC GCA TTC CAG GGG GGG GAC CTC CGT CTC CAC TTC CCT GAG 774
 Lys Asp Cys Ala Phe Gln Gly Gly Asp Leu Arg Leu His Phe Pro Glu
 235 240 245
 TTG GAC TTC ATC AAC GAG AGC CAA GAG CGG CGC ATC GAG AGG CTG GCC 822
 Leu Asp Phe Ile Asn Glu Ser Gln Glu Arg Arg Ile Glu Arg Leu Ala
 250 255 260
 GCC CGC GGC TCC TAC TCC AGA CGC GCC GTC ATT TTC TCC GGC GAC GAC 870
 Ala Arg Gly Ser Tyr Ser Arg Arg Ala Val Ile Phe Ser Gly Asp Asp
 265 270 275
 GAC TGG GGT GAT GCG TAC TTA CAC GAC TTC CAC ACA TGG CTC GCC TAC 918
 Asp Trp Gly Asp Ala Tyr Leu His Asp Phe His Thr Trp Leu Ala Tyr
 280 285 290
 CTA CTG GTG AGG AAC TAC CCC ACT CCG TTT GGT TTC TCA CTC CAT ATA 966
 Leu Leu Val Arg Asn Tyr Pro Thr Pro Phe Gly Phe Ser Leu His Ile
 295 300 305 310
 GAA GTC CAG AGG CGC CAC GGC TCC AGC ATT GAG CTG CGC ATC ACT CGC 1014
 Glu Val Gln Arg Arg His Gly Ser Ser Ile Glu Leu Arg Ile Thr Arg
 315 320 325
 GCG CCA CCT GGA GAC CGC ATG CTG GCC GTC GTC CCA AGG ACG TCC CAA 1062
 Ala Pro Pro Gly Asp Arg Met Leu Ala Val Val Pro Arg Thr Ser Gln
 330 335 340
 GGC CTC TGC AGA ATC CCA AAC ATC TTT TAT TAC GCC GAC GCG TCG GGC 1110
 Gly Leu Cys Arg Ile Pro Asn Ile Phe Tyr Tyr Ala Asp Ala Ser Gly
 345 350 355
 ACT GAG CAT AAG ACC ATC CTT ACG TCA CAG CAC AAA GTC AAC ATG CTG 1158
 Thr Glu His Lys Thr Ile Leu Thr Ser Gln His Lys Val Asn Met Leu
 360 365 370
 CTC AAT TTT ATG CAA ACG CGT CCT GAG AAG GAA CTA GTC GAC ATG ACC 1206
 Leu Asn Phe Met Gln Thr Arg Pro Glu Lys Glu Leu Val Asp Met Thr
 375 380 385 390

GTC TTG ATG TCG TTC GCG CGC GCT AGG CTG CGC GCG ATC GTG GTC GCC 1254
 Val Leu Met Ser Phe Ala Arg Ala Arg Leu Arg Ala Ile Val Val Ala
 395 400 405
 TCA GAA GTC ACC GAG AGC TCC TGG AAC ATC TCA CCG GCT GAC CTG GTC 1302
 Ser Glu Val Thr Glu Ser Ser Trp Asn Ile Ser Pro Ala Asp Leu Val
 410 415 420
 CGC ACT GTC GTG TCT CTT TAC GTC CTC CAC ATC ATC GAG CGC CGA AGG 1350
 Arg Thr Val Val Ser Leu Tyr Val Leu His Ile Ile Glu Arg Arg Arg
 425 430 435
 GCT GCG GTC GCT GTC AAG ACC GCC AAG GAC GAC GTC TTT GGA GAG ACT 1398
 Ala Ala Val Ala Val Lys Thr Ala Lys Asp Asp Val Phe Gly Glu Thr
 440 445 450
 TCG TTC TGG GAG AGT CTC AAG CAC GTC TTG GGC TCC TGT TGC GGT CTG 1446
 Ser Phe Trp Glu Ser Leu Lys His Val Leu Gly Ser Cys Cys Gly Leu
 455 460 465 470
 CGC AAC CTC AAA GGC ACC GAC GTC GTC TTT ACT AAG CGC GTC GTC GAT 1494
 Arg Asn Leu Lys Gly Thr Asp Val Val Phe Thr Lys Arg Val Val Asp
 475 480 485
 AAG TAC CGA GTC CAC CTC GGA GAC ATA ATC TGC GAC GTC CGC CTG 1542
 Lys Tyr Arg Val His Ser Leu Gly Asp Ile Ile Cys Asp Val Arg Leu
 490 495 500
 TCC CCT GAA CAG GTC GGC TTC CTG CCG TCC CGC GTA CCA CCT GCC CGC 1590
 Ser Pro Glu Gln Val Gly Phe Leu Pro Ser Arg Val Pro Pro Ala Arg
 505 510 515
 GTC TTT CAC GAC AGG GAA GAG CTT GAG GTC CTT CGC GAA GCT GGC TGC 1638
 Val Phe His Asp Arg Glu Glu Leu Glu Val Leu Arg Glu Ala Gly Cys
 520 525 530
 TAC AAC GAA CGT CCG GTA CCT TCC ACT CCT CCT GTG GAG GAG CCC CAA 1686
 Tyr Asn Glu Arg Pro Val Pro Ser Thr Pro Pro Val Glu Glu Pro Gln
 535 540 545 550
 GGT TTC GAC GCC GAC TTG TGG CAC GCG ACC GCG GCC TCA CTC CCC GAG 1734
 Gly Phe Asp Ala Asp Leu Trp His Ala Thr Ala Ala Ser Leu Pro Glu
 555 560 565
 TAC CGC GCC ACC TTG CAG GCA GGT CTC AAC ACC GAC GTC AAG CAG CTC 1782
 Tyr Arg Ala Thr Leu Gln Ala Gly Leu Asn Thr Asp Val Lys Gln Leu
 570 575 580
 AAG ATC ACC CTC GAG AAC GCC CTC AAG ACC ATC GAC GGG CTC ACC CTC 1830
 Lys Ile Thr Leu Glu Asn Ala Leu Lys Thr Ile Asp Gly Leu Thr Leu
 585 590 595
 TCC CCA GTC AGA GGC CTC GAG ATG TAC GAG GGC CCG CCA GGC AGC GGC 1878
 Ser Pro Val Arg Gly Leu Glu Met Tyr Glu Gly Pro Pro Gly Ser Gly
 600 605 610
 AAG ACG GGC ACC CTC ATC GCC GCC CTT GAG GCC GCG GGC GGT AAA GCA 1926
 Lys Thr Gly Thr Leu Ile Ala Ala Leu Glu Ala Ala Gly Gly Lys Ala
 615 620 625 630
 CTT TAC GTG GCA CCC ACC AGA GAA CTG AGA GAG GCT ATG GAC CGG CGG 1974
 Leu Tyr Val Ala Pro Thr Arg Glu Leu Arg Glu Ala Met Asp Arg Arg
 635 640 645
 ATC AAA CCG CCG TCC GCC TCG GCT ACG CAA CAT GTC GCC CTT GCG ATT 2022
 Ile Lys Pro Pro Ser Ala Ser Ala Thr Gln His Val Ala Leu Ala Ile
 650 655 660
 CTC CGT CGT GCC ACC GCC GAG GGC GCC CCT TTC GCT ACC GTG GTT ATC 2070
 Leu Arg Arg Ala Thr Ala Glu Gly Ala Pro Phe Ala Thr Val Val Ile
 665 670 675
 GAC GAG TGC TTC ATG TTC CCG CTC GTG TAC GTC GCG ATC GTG CAC GCC 2118
 Asp Glu Cys Phe Met Phe Pro Leu Val Tyr Val Ala Ile Val His Ala
 680 685 690

TTG TCC CCG AGC TCA CGA ATA GTC CTT GTA GGG GAC GTC CAC CAA ATC 2166
 Leu Ser Pro Ser Ser Arg Ile Val Leu Val Gly Asp Val His Gln Ile
 695 700 705 710
 GGG TTT ATA GAC TTC CAA GGC ACA AGC GCG AAC ATG CCG CTC GTT CGC 2214
 Gly Phe Ile Asp Phe Gln Gly Thr Ser Ala Asn Met Pro Leu Val Arg
 715 720 725
 GAC GTC GTT AAG CAG TGC CGT CGG CGC ACT TTC AAC CAA ACC AAG CGC 2262
 Asp Val Val Lys Gln Cys Arg Arg Arg Thr Phe Asn Gln Thr Lys Arg
 730 735 740
 TGT CCG GCC GAC GTC GTT GCC ACC ACG TTT TTC CAG AGC TTG TAC CCC 2310
 Cys Pro Ala Asp Val Val Ala Thr Thr Phe Phe Gln Ser Leu Tyr Pro
 745 750 755
 GGG TGC ACA ACC ACC TCA GGG TGC GTC GCA TCC ATC AGC CAC GTC GCC 2358
 Gly Cys Thr Thr Thr Ser Gly Cys Val Ala Ser Ile Ser His Val Ala
 760 765 770
 CCA GAC TAC CGC AAC AGC CAG GCG CAA ACG CTC TGC TTC ACG CAG GAG 2406
 Pro Asp Tyr Arg Asn Ser Gln Ala Gln Thr Leu Cys Phe Thr Gln Glu
 775 780 785 790
 GAA AAG TCG CGC CAC GGG GCT GAG GGC GCG ATG ACT GTG CAC GAA GCG 2454
 Glu Lys Ser Arg His Gly Ala Glu Gly Ala Met Thr Val His Glu Ala
 795 800 805
 CAG GGA CGC ACT TTT GCG TCT GTC ATT CTG CAT TAC AAC GGC TCC ACA 2502
 Gln Gly Arg Thr Phe Ala Ser Val Ile Leu His Tyr Asn Gly Ser Thr
 810 815 820
 GCA GAG CAG AAG CTC CTC GCT GAG AAG TCG CAC CTT CTA GTC GGC ATC 2550
 Ala Glu Gln Lys Leu Leu Ala Glu Lys Ser His Leu Leu Val Gly Ile
 825 830 835
 ACG CGC CAC ACC AAC CAC CTG TAC ATC CGC GAC CCG ACA GGT GAC ATT 2598
 Thr Arg His Thr Asn His Leu Tyr Ile Arg Asp Pro Thr Gly Asp Ile
 840 845 850
 GAG AGA CAA CTC AAC CAT AGC GCG AAA GCC GAG GTG TTT ACA GAC ATC 2646
 Glu Arg Gln Leu Asn His Ser Ala Lys Ala Glu Val Phe Thr Asp Ile
 855 860 865 870
 CCT GCA CCC CTG GAG ATC ACG ACT GTC AAA CCG AGT GAA GAG GTG CAG 2694
 Pro Ala Pro Leu Glu Ile Thr Thr Val Lys Pro Ser Glu Glu Val Gln
 875 880 885
 CGC AAC GAA GTG ATG GCA ACG ATA CCC CCG CAG AGT GCC ACG CCG CAC 2742
 Arg Asn Glu Val Met Ala Thr Ile Pro Pro Gln Ser Ala Thr Pro His
 890 895 900
 GGA GCA ATC CAT CTG CTC CGC AAG AAC TTC GGG GAC CAA CCC GAC TGT 2790
 Gly Ala Ile His Leu Leu Arg Lys Asn Phe Gly Asp Gln Pro Asp Cys
 905 910 915
 GGC TGT GTC GCT TTG GCG AAG ACC GGC TAC GAG GTG TTT GGC GGT CGT 2838
 Gly Cys Val Ala Leu Ala Lys Thr Gly Tyr Glu Val Phe Gly Gly Arg
 920 925 930
 GCC AAA ATC AAC GTA GAG CTT GCC GAA CCC GAC GCG ACC CCG AAG CCG 2886
 Ala Lys Ile Asn Val Glu Leu Ala Glu Pro Asp Ala Thr Pro Lys Pro
 935 940 945 950
 CAT AGG GCG TTC CAG GAA GGG GTA CAG TGG GTC AAG GTC ACC AAC GCG 2934
 His Arg Ala Phe Gln Glu Gly Val Gln Trp Val Lys Val Thr Asn Ala
 955 960 965
 TCT AAC AAA CAC CAG GCG CTC CAG ACG CTG TTG TCC CGC TAC ACC AAG 2982
 Ser Asn Lys His Gln Ala Leu Gln Thr Leu Leu Ser Arg Tyr Thr Lys
 970 975 980
 CGA AGC GCT GAC CTG CCG CTA CAC GAA GCT AAG GAG GAC GTC AAA CGC 3030
 Arg Ser Ala Asp Leu Pro Leu His Glu Ala Lys Glu Asp Val Lys Arg
 985 990 995

ATG CTA AAC TCG CTT GAC CGA CAT TGG GAC TGG ACT GTC ACT GAA GAC 3078
 Met Leu Asn Ser Leu Asp Arg His Trp Asp Trp Thr Val Thr Glu Asp
 1000 1005 1010
 GCC CGT GAC CGA GCT GTC TTC GAG ACC CAG CTC AAG TTC ACC CAA CGC 3126
 Ala Arg Asp Arg Ala Val Phe Glu Thr Gln Leu Lys Phe Thr Gln Arg
 1015 1020 1025 1030
 GGC GGC ACC GTC GAA GAC CTG CTG GAG CCA GAC GAC CCC TAC ATC CGT 3174
 Gly Gly Thr Val Glu Asp Leu Leu Glu Pro Asp Asp Pro Tyr Ile Arg
 1035 1040 1045
 GAC ATA GAC TTC CTT ATG AAG ACT CAG CAG AAA GTG TCG CCC AAG CCG 3222
 Asp Ile Asp Phe Leu Met Lys Thr Gln Gln Lys Val Ser Pro Lys Pro
 1050 1055 1060
 ATC AAT ACG GGC AAG GTC GGG CAG GGG ATC GCC GCT CAC TCA AAG TCT 3270
 Ile Asn Thr Gly Lys Val Gly Gln Gly Ile Ala Ala His Ser Lys Ser
 1065 1070 1075
 CTC AAC TTC GTC CTC GCC GCT TGG ATA CGC ATA CTC GAG GAG ATA CTC 3318
 Leu Asn Phe Val Leu Ala Ala Trp Ile Arg Ile Leu Glu Glu Ile Leu
 1080 1085 1090
 CGT ACC GGG AGC CGC ACG GTC CGG TAC AGC AAC GGT CTC CCC GAC GAA 3366
 Arg Thr Gly Ser Arg Thr Val Arg Tyr Ser Asn Gly Leu Pro Asp Glu
 1095 1100 1105 1110
 GAA GAG GCC ATG CTG CTC GAA GCG AAG ATC AAT CAA GTC CCA CAC GCC 3414
 Glu Glu Ala Met Leu Leu Glu Ala Lys Ile Asn Gln Val Pro His Ala
 1115 1120 1125
 ACG TTC GTC TCG GCG GAC TGG ACC GAG TTT GAC ACC GCC CAC AAT AAC 3462
 Thr Phe Val Ser Ala Asp Trp Thr Glu Phe Asp Thr Ala His Asn Asn
 1130 1135 1140
 ACG AGT GAG CTG CTC TTC GCC GCC CTT TTA GAG CGC ATC GGC ACG CCT 3510
 Thr Ser Glu Leu Leu Phe Ala Ala Leu Leu Glu Arg Ile Gly Thr Pro
 1145 1150 1155
 GCA GCT GCC GTT AAT CTA TTC AGA GAA CGG TGT GGG AAA CGC ACC TTG 3558
 Ala Ala Ala Val Asn Leu Phe Arg Glu Arg Cys Gly Lys Arg Thr Leu
 1160 1165 1170
 CGA GCG AAG GGT CTA GGC TCC GTT GAA GTC GAC GGT CTG CTC GAC TCC 3606
 Arg Ala Lys Gly Leu Gly Ser Val Glu Val Asp Gly Leu Leu Asp Ser
 1175 1180 1185 1190
 GGC GCA GCT TGG ACG CCT TGC CGC AAC ACC ATC TTC TCT GCC GCC GTC 3654
 Gly Ala Ala Trp Thr Pro Cys Arg Asn Thr Ile Phe Ser Ala Ala Val
 1195 1200 1205
 ATG CTC ACG CTC TTC CGC GGC GTC AAG TTC GCA GCT TTC AAA GGC GAC 3702
 Met Leu Thr Leu Phe Arg Gly Val Lys Phe Ala Ala Phe Lys Gly Asp
 1210 1215 1220
 GAC TCG CTC CTC TGT GGT AGC CAT TAC CTC CGT TTC GAC GCT AGC CGC 3750
 Asp Ser Leu Leu Cys Gly Ser His Tyr Leu Arg Phe Asp Ala Ser Arg
 1225 1230 1235
 CTT CAC ATG GGC GAA CGT TAC AAG ACC AAA CAT TTG AAG GTC GAG GTG 3798
 Leu His Met Gly Glu Arg Tyr Lys Thr Lys His Leu Lys Val Glu Val
 1240 1245 1250
 CAG AAA ATC GTG CCG TAC ATC GGA CTC CTC GTC TCC GCT GAG CAG GTC 3846
 Gln Lys Ile Val Pro Tyr Ile Gly Leu Leu Val Ser Ala Glu Gln Val
 1255 1260 1265 1270
 GTC CTC GAC CCT GTC AGG AGC GCT CTC AAG ATA TTT GGG CGC TGC TAC 3894
 Val Leu Asp Pro Val Arg Ser Ala Leu Lys Ile Phe Gly Arg Cys Tyr
 1275 1280 1285
 ACA AGC GAA CTC CTT TAC TCC AAG TAC GTG GAG GCT GTG AGA GAC ATC 3942
 Thr Ser Glu Leu Leu Tyr Ser Lys Tyr Val Glu Ala Val Arg Asp Ile
 1290 1295 1300

ACC AAG GGC TGG AGT GAC GCC CGC TAC CAC AGC CTC CTG TGC CAC ATG 3990
Thr Lys Gly Trp Ser Asp Ala Arg Tyr His Ser Leu Leu Cys His Met
1305 1310 1315

TCA GCA TGC TAC TAC AAT TAC GCG CCG GAG TCT GCG GCG TAC ATC ATC 4038
Ser Ala Cys Tyr Tyr Asn Tyr Ala Pro Glu Ser Ala Ala Tyr Ile Ile
1320 1325 1330

GAC GCT GTT GTT CGC TTT GGG CGC GGC GAC TTC CCG TTT GAA CAA CTG 4086
Asp Ala Val Val Arg Phe Gly Arg Gly Asp Phe Pro Phe Glu Gln Leu
1335 1340 1345 1350

CGC GTG GTG CGT GCC CAT GTG CAG GCA CCC GAC GCT TAC AGC AGC ACG 4134
Arg Val Val Arg Ala His Val Gln Ala Pro Asp Ala Tyr Ser Ser Thr
1355 1360 1365

TAT CCG GCT AAC GTG CGC GCA TCG TGC CTT GAC CAC GTC TTC GAG CCC 4182
Tyr Pro Ala Asn Val Arg Ala Ser Cys Leu Asp His Val Phe Glu Pro
1370 1375 1380

CGC CAG GCC GCC GCC CCG GCA GGT TTC GTT GCG ACA TGT GCG AAG CCG 4230
Arg Gln Ala Ala Ala Pro Ala Gly Phe Val Ala Thr Cys Ala Lys Pro
1385 1390 1395

GAA ACG CCT TCT TCA CTT ACC GCG AAA GCT GGT GTT TCT GCG ACT ACA 4278
Glu Thr Pro Ser Ser Leu Thr Ala Lys Ala Gly Val Ser Ala Thr Thr
1400 1405 1410

AGC CAC GTT GCG ACT GGG ACT GCG CCC CCG GAG TCT CCA TGG GAT GCA 4326
Ser His Val Ala Thr Gly Thr Ala Pro Pro Glu Ser Pro Trp Asp Ala
1415 1420 1425 1430

CCT GCA GCC AAC AGC TTT TCG GAG TTA TTG ACA CCG GAG ACC CCG TCC 4374
Pro Ala Ala Asn Ser Phe Ser Glu Leu Leu Thr Pro Glu Thr Pro Ser
1435 1440 1445

ACA TCA TCC TCG CCG TCA TCG TCT TCA TCG GAC TCC TCT ACA TCG TGT 4422
Thr Ser Ser Ser Pro Ser Ser Ser Ser Ser Asp Ser Ser Thr Ser Cys
1450 1455 1460

GGA AGG TCG CTC AGT GGT GGA GAC ACC GCA AGG ACC ACA GAA GAC TTG 4470
Gly Arg Ser Leu Ser Gly Gly Asp Thr Ala Arg Thr Thr Glu Asp Leu
1465 1470 1475

AAC AGC AGA AAG CCG CCT TCG CAA GAC AGG CAA TCA CGC TCG TCT GAA 4518
Asn Ser Arg Lys Pro Pro Ser Gln Asp Arg Gln Ser Arg Ser Ser Glu
1480 1485 1490

TGT CTG GAC AGA AGC GGA GAA AGG ACA GGC AGT TCG TTA ACT GCC CCC 4566
Cys Leu Asp Arg Ser Gly Glu Arg Thr Gly Ser Ser Leu Thr Ala Pro
1495 1500 1505 1510

ACT GCT CCG AGC CCC TCA TTC TCA TTT TCG GAA AGA GCT CGA CTG GCG 4614
Thr Ala Pro Ser Pro Ser Phe Ser Phe Ser Glu Arg Ala Arg Leu Ala
1515 1520 1525

ACC GGG CCG ACT GTC GCC GCT GCG ACA TCA CCT TCG GCA ACC CCA TCC 4662
Thr Gly Pro Thr Val Ala Ala Ala Thr Ser Pro Ser Ala Thr Pro Ser
1530 1535 1540

TGC GCC ACG GAC CAG GTT GCC GCG AGG ACC ACG CCG GAC TTT GCG CCT 4710
Cys Ala Thr Asp Gln Val Ala Ala Arg Thr Thr Pro Asp Phe Ala Pro
1545 1550 1555

TTC CTG GGT TCC CAG TCT GCC CGT GCT GTC TCG AAG CCG TAC CGG CCC 4758
Phe Leu Gly Ser Gln Ser Ala Arg Ala Val Ser Lys Pro Tyr Arg Pro
1560 1565 1570

CCC ACG ACT GCC CGT TGG AAA GAA GTC ACC CCG CTC CAC GCG TGG AAG 4806
Pro Thr Thr Ala Arg Trp Lys Glu Val Thr Pro Leu His Ala Trp Lys
1575 1580 1585 1590

GGC GTG ACC GGA GAC CGA CCG GAA GTC AGG GAG GAC CCG GAG ACA GCG 4854
Gly Val Thr Gly Asp Arg Pro Glu Val Arg Glu Asp Pro Glu Thr Ala
1595 1600 1605

GCG GTC GTC CAG GCT CTG ATC AGC GGC CGT TAT CCT CAG AAG ACG AAG 4902
 Ala Val Val Gln Ala Leu Ile Ser Gly Arg Tyr Pro Gln Lys Thr Lys
 1610 1615 1620
 CTT TCC TCC GAC GCA TCC AAA GGC TAC TCA AGA ACT AAG GGA TGC TCA 4950
 Leu Ser Ser Asp Ala Ser Lys Gly Tyr Ser Arg Thr Lys Gly Cys Ser
 1625 1630 1635
 CAA TCC ACC TCT TTT CCT GCC CCG AGT GCG GAT TAC CAG GCC CGC GAC 4998
 Gln Ser Thr Ser Phe Pro Ala Pro Ser Ala Asp Tyr Gln Ala Arg Asp
 1640 1645 1650
 TGC CAG ACA GTC CGA GTC TGC CGC GCC GCT GCA GAG ATG GCG CGC TCA 5046
 Cys Gln Thr Val Arg Val Cys Arg Ala Ala Ala Glu Met Ala Arg Ser
 1655 1660 1665 1670
 TGT ATT CAC GAG CCG TTG GCT TCA TCT GCC GCC AGT GCC GAC TTG AAG 5094
 Cys Ile His Glu Pro Leu Ala Ser Ser Ala Ala Ser Ala Asp Leu Lys
 1675 1680 1685
 CGC ATA CGC TCT ACC TCG GAC TCT GTT CCC GAT GTA AAG ATC AGC AAG 5142
 Arg Ile Arg Ser Thr Ser Asp Ser Val Pro Asp Val Lys Ile Ser Lys
 1690 1695 1700
 AGC GCA TGAAGGAACA AAATTAGTTT CCTTGTTTCGT AAACAAGGTG GTCCCTCCCA 5198
 Ser Ala

 TTGAGGTAAA GACTCTGGTG AGTCCTCAAC GTTACTCGTT GAGTCTGCTG CGGTTTCGATT 5258
 CCATTCCCAA GCAGCAAAGG GTGCGCAACT AGTACGGCGC CCCCTGGGAT ACCA 5312

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1704 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Tyr Ala Lys Ala Thr Asp Val Ala Arg Val Tyr Ala Ala Ala Asp
 1 5 10 15
 Val Ala Tyr Ala Asn Val Leu Gln Gln Arg Ala Val Lys Leu Asp Phe
 20 25 30
 Ala Pro Pro Leu Lys Ala Leu Glu Thr Leu His Arg Leu Tyr Tyr Pro
 35 40 45
 Leu Arg Phe Lys Gly Gly Thr Leu Pro Pro Thr Gln His Pro Ile Leu
 50 55 60
 Ala Gly His Gln Arg Val Ala Glu Glu Val Leu His Asn Phe Ala Arg
 65 70 75 80
 Gly Arg Ser Thr Val Leu Glu Ile Gly Pro Ser Leu His Ser Ala Leu
 85 90 95
 Lys Leu His Gly Ala Pro Asn Ala Pro Val Ala Asp Tyr His Gly Cys
 100 105 110
 Thr Lys Tyr Gly Thr Arg Asp Gly Ser Arg His Ile Thr Ala Leu Glu
 115 120 125
 Ser Arg Ser Val Ala Thr Gly Arg Pro Glu Phe Lys Ala Asp Ala Ser
 130 135 140
 Leu Leu Ala Asn Gly Ile Ala Ser Arg Thr Phe Cys Val Asp Gly Val
 145 150 155 160
 Gly Ser Cys Ala Phe Lys Ser Arg Val Gly Ile Ala Asn His Ser Leu
 165 170 175
 Tyr Asp Val Thr Leu Glu Glu Leu Ala Asn Ala Phe Glu Asn His Gly
 180 185 190
 Leu His Met Val Arg Ala Phe Met His Met Pro Glu Glu Leu Leu Tyr

195 200 205
 Met Asp Asn Val Val Asn Ala Glu Leu Gly Tyr Arg Phe His Val Ile
 210 215 220
 Glu Glu Pro Met Ala Val Lys Asp Cys Ala Phe Gln Gly Gly Asp Leu
 225 230 235 240
 Arg Leu His Phe Pro Glu Leu Asp Phe Ile Asn Glu Ser Gln Glu Arg
 245 250 255
 Arg Ile Glu Arg Leu Ala Ala Arg Gly Ser Tyr Ser Arg Arg Ala Val
 260 265 270
 Ile Phe Ser Gly Asp Asp Asp Trp Gly Asp Ala Tyr Leu His Asp Phe
 275 280 285
 His Thr Trp Leu Ala Tyr Leu Leu Val Arg Asn Tyr Pro Thr Pro Phe
 290 295 300
 Gly Phe Ser Leu His Ile Glu Val Gln Arg Arg His Gly Ser Ser Ile
 305 310 315 320
 Glu Leu Arg Ile Thr Arg Ala Pro Pro Gly Asp Arg Met Leu Ala Val
 325 330 335
 Val Pro Arg Thr Ser Gln Gly Leu Cys Arg Ile Pro Asn Ile Phe Tyr
 340 345 350
 Tyr Ala Asp Ala Ser Gly Thr Glu His Lys Thr Ile Leu Thr Ser Gln
 355 360 365
 His Lys Val Asn Met Leu Leu Asn Phe Met Gln Thr Arg Pro Glu Lys
 370 375 380
 Glu Leu Val Asp Met Thr Val Leu Met Ser Phe Ala Arg Ala Arg Leu
 385 390 395 400
 Arg Ala Ile Val Val Ala Ser Glu Val Thr Glu Ser Ser Trp Asn Ile
 405 410 415
 Ser Pro Ala Asp Leu Val Arg Thr Val Val Ser Leu Tyr Val Leu His
 420 425 430
 Ile Ile Glu Arg Arg Arg Ala Ala Val Ala Val Lys Thr Ala Lys Asp
 435 440 445
 Asp Val Phe Gly Glu Thr Ser Phe Trp Glu Ser Leu Lys His Val Leu
 450 455 460
 Gly Ser Cys Cys Gly Leu Arg Asn Leu Lys Gly Thr Asp Val Val Phe
 465 470 475 480
 Thr Lys Arg Val Val Asp Lys Tyr Arg Val His Ser Leu Gly Asp Ile
 485 490 495
 Ile Cys Asp Val Arg Leu Ser Pro Glu Gln Val Gly Phe Leu Pro Ser
 500 505 510
 Arg Val Pro Pro Ala Arg Val Phe His Asp Arg Glu Glu Leu Glu Val
 515 520 525
 Leu Arg Glu Ala Gly Cys Tyr Asn Glu Arg Pro Val Pro Ser Thr Pro
 530 535 540
 Pro Val Glu Glu Pro Gln Gly Phe Asp Ala Asp Leu Trp His Ala Thr
 545 550 555 560
 Ala Ala Ser Leu Pro Glu Tyr Arg Ala Thr Leu Gln Ala Gly Leu Asn
 565 570 575
 Thr Asp Val Lys Gln Leu Lys Ile Thr Leu Glu Asn Ala Leu Lys Thr
 580 585 590
 Ile Asp Gly Leu Thr Leu Ser Pro Val Arg Gly Leu Glu Met Tyr Glu
 595 600 605
 Gly Pro Pro Gly Ser Gly Lys Thr Gly Thr Leu Ile Ala Ala Leu Glu
 610 615 620
 Ala Ala Gly Gly Lys Ala Leu Tyr Val Ala Pro Thr Arg Glu Leu Arg
 625 630 635 640
 Glu Ala Met Asp Arg Arg Ile Lys Pro Pro Ser Ala Ser Ala Thr Gln
 645 650 655

His Val Ala Leu Ala Ile Leu Arg Arg Ala Thr Ala Glu Gly Ala Pro
 660 665 670
 Phe Ala Thr Val Val Ile Asp Glu Cys Phe Met Phe Pro Leu Val Tyr
 675 680 685
 Val Ala Ile Val His Ala Leu Ser Pro Ser Ser Arg Ile Val Leu Val
 690 695 700
 Gly Asp Val His Gln Ile Gly Phe Ile Asp Phe Gln Gly Thr Ser Ala
 705 710 715 720
 Asn Met Pro Leu Val Arg Asp Val Val Lys Gln Cys Arg Arg Arg Thr
 725 730 735
 Phe Asn Gln Thr Lys Arg Cys Pro Ala Asp Val Val Ala Thr Thr Phe
 740 745 750
 Phe Gln Ser Leu Tyr Pro Gly Cys Thr Thr Thr Ser Gly Cys Val Ala
 755 760 765
 Ser Ile Ser His Val Ala Pro Asp Tyr Arg Asn Ser Gln Ala Gln Thr
 770 775 780
 Leu Cys Phe Thr Gln Glu Glu Lys Ser Arg His Gly Ala Glu Gly Ala
 785 790 795 800
 Met Thr Val His Glu Ala Gln Gly Arg Thr Phe Ala Ser Val Ile Leu
 805 810 815
 His Tyr Asn Gly Ser Thr Ala Glu Gln Lys Leu Leu Ala Glu Lys Ser
 820 825 830
 His Leu Leu Val Gly Ile Thr Arg His Thr Asn His Leu Tyr Ile Arg
 835 840 845
 Asp Pro Thr Gly Asp Ile Glu Arg Gln Leu Asn His Ser Ala Lys Ala
 850 855 860
 Glu Val Phe Thr Asp Ile Pro Ala Pro Leu Glu Ile Thr Thr Val Lys
 865 870 875 880
 Pro Ser Glu Glu Val Gln Arg Asn Glu Val Met Ala Thr Ile Pro Pro
 885 890 895
 Gln Ser Ala Thr Pro His Gly Ala Ile His Leu Leu Arg Lys Asn Phe
 900 905 910
 Gly Asp Gln Pro Asp Cys Gly Cys Val Ala Leu Ala Lys Thr Gly Tyr
 915 920 925
 Glu Val Phe Gly Gly Arg Ala Lys Ile Asn Val Glu Leu Ala Glu Pro
 930 935 940
 Asp Ala Thr Pro Lys Pro His Arg Ala Phe Gln Glu Gly Val Gln Trp
 945 950 955 960
 Val Lys Val Thr Asn Ala Ser Asn Lys His Gln Ala Leu Gln Thr Leu
 965 970 975
 Leu Ser Arg Tyr Thr Lys Arg Ser Ala Asp Leu Pro Leu His Glu Ala
 980 985 990
 Lys Glu Asp Val Lys Arg Met Leu Asn Ser Leu Asp Arg His Trp Asp
 995 1000 1005
 Trp Thr Val Thr Glu Asp Ala Arg Asp Arg Ala Val Phe Glu Thr Gln
 1010 1015 1020
 Leu Lys Phe Thr Gln Arg Gly Gly Thr Val Glu Asp Leu Leu Glu Pro
 1025 1030 1035 1040
 Asp Asp Pro Tyr Ile Arg Asp Ile Asp Phe Leu Met Lys Thr Gln Gln
 1045 1050 1055
 Lys Val Ser Pro Lys Pro Ile Asn Thr Gly Lys Val Gly Gln Gly Ile
 1060 1065 1070
 Ala Ala His Ser Lys Ser Leu Asn Phe Val Leu Ala Ala Trp Ile Arg
 1075 1080 1085
 Ile Leu Glu Glu Ile Leu Arg Thr Gly Ser Arg Thr Val Arg Tyr Ser
 1090 1095 1100
 Asn Gly Leu Pro Asp Glu Glu Glu Ala Met Leu Leu Glu Ala Lys Ile

1105 1110 1115 1120
 Asn Gln Val Pro His Ala Thr Phe Val Ser Ala Asp Trp Thr Glu Phe
 1125 1130 1135
 Asp Thr Ala His Asn Asn Thr Ser Glu Leu Leu Phe Ala Ala Leu Leu
 1140 1145 1150
 Glu Arg Ile Gly Thr Pro Ala Ala Ala Val Asn Leu Phe Arg Glu Arg
 1155 1160 1165
 Cys Gly Lys Arg Thr Leu Arg Ala Lys Gly Leu Gly Ser Val Glu Val
 1170 1175 1180
 Asp Gly Leu Leu Asp Ser Gly Ala Ala Trp Thr Pro Cys Arg Asn Thr
 1185 1190 1195 1200
 Ile Phe Ser Ala Ala Val Met Leu Thr Leu Phe Arg Gly Val Lys Phe
 1205 1210 1215
 Ala Ala Phe Lys Gly Asp Asp Ser Leu Leu Cys Gly Ser His Tyr Leu
 1220 1225 1230
 Arg Phe Asp Ala Ser Arg Leu His Met Gly Glu Arg Tyr Lys Thr Lys
 1235 1240 1245
 His Leu Lys Val Glu Val Gln Lys Ile Val Pro Tyr Ile Gly Leu Leu
 1250 1255 1260
 Val Ser Ala Glu Gln Val Val Leu Asp Pro Val Arg Ser Ala Leu Lys
 1265 1270 1275 1280
 Ile Phe Gly Arg Cys Tyr Thr Ser Glu Leu Leu Tyr Ser Lys Tyr Val
 1285 1290 1295
 Glu Ala Val Arg Asp Ile Thr Lys Gly Trp Ser Asp Ala Arg Tyr His
 1300 1305 1310
 Ser Leu Leu Cys His Met Ser Ala Cys Tyr Tyr Asn Tyr Ala Pro Glu
 1315 1320 1325
 Ser Ala Ala Tyr Ile Ile Asp Ala Val Val Arg Phe Gly Arg Gly Asp
 1330 1335 1340
 Phe Pro Phe Glu Gln Leu Arg Val Val Arg Ala His Val Gln Ala Pro
 1345 1350 1355 1360
 Asp Ala Tyr Ser Ser Thr Tyr Pro Ala Asn Val Arg Ala Ser Cys Leu
 1365 1370 1375
 Asp His Val Phe Glu Pro Arg Gln Ala Ala Pro Ala Gly Phe Val
 1380 1385 1390
 Ala Thr Cys Ala Lys Pro Glu Thr Pro Ser Ser Leu Thr Ala Lys Ala
 1395 1400 1405
 Gly Val Ser Ala Thr Thr Ser His Val Ala Thr Gly Thr Ala Pro Pro
 1410 1415 1420
 Glu Ser Pro Trp Asp Ala Pro Ala Ala Asn Ser Phe Ser Glu Leu Leu
 1425 1430 1435 1440
 Thr Pro Glu Thr Pro Ser Thr Ser Ser Ser Pro Ser Ser Ser Ser
 1445 1450 1455
 Asp Ser Ser Thr Ser Cys Gly Arg Ser Leu Ser Gly Gly Asp Thr Ala
 1460 1465 1470
 Arg Thr Thr Glu Asp Leu Asn Ser Arg Lys Pro Pro Ser Gln Asp Arg
 1475 1480 1485
 Gln Ser Arg Ser Ser Glu Cys Leu Asp Arg Ser Gly Glu Arg Thr Gly
 1490 1495 1500
 Ser Ser Leu Thr Ala Pro Thr Ala Pro Ser Pro Ser Phe Ser Phe Ser
 1505 1510 1515 1520
 Glu Arg Ala Arg Leu Ala Thr Gly Pro Thr Val Ala Ala Ala Thr Ser
 1525 1530 1535
 Pro Ser Ala Thr Pro Ser Cys Ala Thr Asp Gln Val Ala Ala Arg Thr
 1540 1545 1550
 Thr Pro Asp Phe Ala Pro Phe Leu Gly Ser Gln Ser Ala Arg Ala Val
 1555 1560 1565

Ser Lys Pro Tyr Arg Pro Pro Thr Thr Ala Arg Trp Lys Glu Val Thr
 1570 1575 1580
 Pro Leu His Ala Trp Lys Gly Val Thr Gly Asp Arg Pro Glu Val Arg
 1585 1590 1595 1600
 Glu Asp Pro Glu Thr Ala Ala Val Val Gln Ala Leu Ile Ser Gly Arg
 1605 1610 1615
 Tyr Pro Gln Lys Thr Lys Leu Ser Ser Asp Ala Ser Lys Gly Tyr Ser
 1620 1625 1630
 Arg Thr Lys Gly Cys Ser Gln Ser Thr Ser Phe Pro Ala Pro Ser Ala
 1635 1640 1645
 Asp Tyr Gln Ala Arg Asp Cys Gln Thr Val Arg Val Cys Arg Ala Ala
 1650 1655 1660
 Ala Glu Met Ala Arg Ser Cys Ile His Glu Pro Leu Ala Ser Ser Ala
 1665 1670 1675 1680
 Ala Ser Ala Asp Leu Lys Arg Ile Arg Ser Thr Ser Asp Ser Val Pro
 1685 1690 1695
 Asp Val Lys Ile Ser Lys Ser Ala
 1700

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 4218..4512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTTCCTGCCTC CCCCAGGACGG TAAATATAGG GGAACAATGT ACGCGAAAGC GACAGACGTG 60
 GCGCGTGTCT ACGCCGCGGC AGATGTCGCC TACGCGAAGC TACTGCAGCA GAGAGCAGTC 120
 AAGTTGGACT TCGCCCCGCC ACTGAAGGCA CTAGAAACCC TCCACAGACT GTACTATCCG 180
 CTGCGCTTCA AAGGGGGCAC TTTACCCCG ACACAACACC CGATCCTGGC CGGGCACCAA 240
 CGTGTGCGAG AAGAGGTTCT GCACAATTTT GCCAGGGGAC GTAGCACAGT GCTCGAGATA 300
 GGGCCGTCTC TGCACAGCGC ACTTAAGCTA CATGGGGCAC CGAACGCCCC CGTCGCAGAC 360
 TATCACGGGT GCACCAAGTA CGGCACCCGC GACGGCTCGC GACACATTAC GGCCTTAGAG 420
 TCTAGATCCG TCGCCACAGG CCGGCCCGAG TTCAAGGCCG ACGCCTCACT GCTCGCCAAC 480
 GGCATTGCCT CCCGCACCTT CTGCGTCGAC GGAGTCGGCT CTTGCGCGTT CAAATCGCGC 540
 GTTGAATTG CCAATCACTC CCTCTATGAC GTGACCCTAG AGGAGCTGGC CAATGCGTTT 600
 GAGAACCACG GACTTCACAT GGTCGCGCG TTCATGCACA TGCCAGAAGA GCTGCTCTAC 660
 ATGGACAACG TGGTTAATGC CGAGCTCGGC TACCGCTTCC ACGTTATTGA AGAGCCTATG 720
 GCTGTGAAGG ACTGCGCATT CCAGGGGGGG GACCTCCGTC TCCACTTCCC TGAGTTGGAC 780
 TTCATCAACG AGAGCCAAGA GCGGCGCATC GAGAGGCTGG CCGCCCGCGG CTCCTACTCC 840
 AGACGCGCCG TCATTTTCTC CGGCGACGAC GACTGGGGTG ATGCGTACTT ACACGACTTC 900
 CACACATGGC TCGCCTACCT ACTGGTGAGG AACTACCCCA CTCCGTTTGG TTTCTCACTC 960
 CATATAGAAG TCCAGAGGCG CCACGGCTCC AGCATTTAGC TGCGCATCAC TCGCGCGCCA 1020
 CCTGGAGACC GCATGCTGGC CGTCGTCCCA AGGAGTCCC AAGGCCTCTG CAGAATCCCA 1080
 AACATCTTTT ATTACGCCGA CGCGTCGGGC ACTGAGCATA AGACCATCCT TACGTCACAG 1140
 CACAAAGTCA ACATGCTGCT CAATTTTATG CAAACGCGTC CTGAGAAGGA ACTAGTCGAC 1200
 ATGACCGTCT TGATGTCGTT CGCGCGCGCT AGGCTGCGCG CGATCGTGGT CGCCTCAGAA 1260
 GTCACCGAGA GCTCCTGGAA CATCTACCG GCTGACCTGG TCCGCACTGT CGTGTCTCTT 1320
 TACGTCTCTC ACATCATCGA GCGCCGAAGG GCTGCGGTCT CTGTCAAGAC CGCCAAGGAC 1380
 GACGTCTTTG GAGAGACTTC GTTCTGGGAG AGTCTCAAGC ACGTCTTGGG CTCCTGTTGC 1440
 GGTCTGCGCA ACCTCAAAGG CACCGACGTC GTCTTTACTA AGCGCGTCGT CGATAAGTAC 1500

CGAGTCCACT CGCTCGGAGA CATAATCTGC GACGTCCGCC TGTCCCCTGA ACAGGTCCGGC 1560
TTCCTGCCGT CCCGCGTACC ACCTGCCCCG GTCTTTTACG ACAGGGAAGA GCTTGAGGTC 1620
CTTCGCGAAG CTGGCTGCTA CAACGAACGT CCGGTACCTT CCACTCCTCC TGTGGAGGAG 1680
CCCCAAGGTT TCGACGCCGA CTTGTGGCAC GCGACCGCGG CCTCACTCCC CGAGTACCGC 1740
GCCACCTTGC AGGCAGGTCT CAACACCGAC GTCAAGCAGC TCAAGATCAC CCTCGAGAAC 1800
GCCCTCAAGA CCATCGACGG GCTCACCCTC TCCCCAGTCA GAGGCCTCGA GATGTACGAG 1860
GGCCCCGCCAG GCAGCGGCAA GACGGGCACC CTCATCGCCG CCCTTGAGGC CGCGGGCGGT 1920
AAAGCACTTT ACGTGGCACC CACCAGAGAA CTGAGAGAGG CTATGGACCG GCGGATCAAA 1980
CCGCCGTCCG CCTCGGCTAC GCAACATGTC GCCCTTGCGA TTCTCCGTCC TGCCACCGCC 2040
GAGGGCGCCC CTTTCGCTAC CGTGGTTATC GACGAGTGCT TCATGTTCCC GCTCGTGTAC 2100
GTGCGGATCG TGCACGCCTT GTCCCCGAGC TCACGAATAG TCCTTGTAGG GGACGTCCAC 2160
CAAATCGGGT TTATAGACTT CCAAGGCACA AGCGCGAACA TGCCGCTCGT TCGCGACGTC 2220
GTTAAGCAGT GCCGTCGGCG CACTTTTCAAC CAAACCAAGC GCTGTCCGGC CGACGTCGTT 2280
GCCACCACGT TTTTCCAGAG CTTGTACCCC GGGTGCACAA CCACCTCAGG GTGCGTCGCA 2340
TCCATCAGCC ACGTCGCCCC AGACTACCGC AACAGCCAGG CGCAAACGCT CTGCTTCACG 2400
CAGGAGGAAA AGTCGCGCCA CGGGGCTGAG GCGCGATGA CTGTGCACGA AGCGCAGGGA 2460
CGCACTTTTG CGTCTGTCTT TCTGCATTAC AACGGCTCCA CAGCAGAGCA GAAGCTCCTC 2520
GCTGAGAAGT CGCACCTTCT AGTCGGCATC ACGCGCCACA CCAACCACCT GTACATCCGC 2580
GACCCGACAG GTGACATTGA GAGACAACCT AACCATAGCG CGAAAGCCGA GGTGTTTACA 2640
GACATCCCTG CACCCCTGGA GATCACGACT GTCAAACCGA GTGAAGAGGT GCAGCGCAAC 2700
GAAGTGATGG CAACGATACC CCCGCAGAGT GCCACGCCGC ACGGAGCAAT CCATCTGCTC 2760
CGCAAGAACT TCGGGGACCA ACCCGACTGT GGCTGTGTCG CTTTGCGCAA GACCGGCTAC 2820
GAGGTGTTTG GCGGTCGTGC CAAAATCAAC GTAGAGCTTG CCGAACCCGA CGCGACCCCG 2880
AAGCCGCATA GGGCGTTCCA GGAAGGGGTA CAGTGGGTCA AGGTCACCAA CGCGTCTAAC 2940
AAACACCAGG CGCTCCAGAC GCTGTTGTCC CGCTACACCA AGCGAAGCGC TGACCTGCCG 3000
CTACACGAAG CTAAGGAGGA CGTCAAACGC ATGCTAAACT CGCTTGACCG ACATTGGGAC 3060
TGGACTGTCA CTGAAGACGC CCGTGACCGA GCTGTCTTCG AGACCCAGCT CAAGTTCACC 3120
CAACGCGGCG GCACCGTCGA AGACCTGCTG GAGCCAGACG ACCCCTACAT CCGTGACATA 3180
GACTTCCTTA TGAAGACTCA GCAGAAAGTG TCGCCCAAGC CGATCAATAC GGGCAAGGTC 3240
GGGCAGGGGA TCGCCGCTCA CTCAAAGTCT CTCAACTTCG TCCTCGCCGC TTGGATACGC 3300
ATACTCGAGG AGATACTCCG TACCGGGAGC CGCACGGTCC GGTACAGCAA CGGTCTCCCC 3360
GACGAAGAAG AGGCCATGCT GCTCGAAGCG AAGATCAATC AAGTCCCACA CGCCACGTTT 3420
GTCTCGGCGG ACTGGACCGA GTTTGACACC GCCCACAATA ACACGAGTGA GCTGCTCTTC 3480
GCCGCCCTTT TAGAGCGCAT CGGCACGCCCT CGAGCTGCCG TTAATCTATT CAGAGAACCG 3540
TGTGGGAAAC GCACCTTGCG AGCGAAGGGT CTAGGCTCCG TTGAAGTCGA CGGTCTGCTC 3600
GACTCCGGCG CAGCTTGAC GCCTTGCCGC AACACCATCT TCTCTGCCGC CGTCATGCTC 3660
ACGCTCTTCC GCGGCGTCAA GTTCGCAGCT TTCAAAGGCG ACGACTCGCT CCTCTGTGGT 3720
AGCCATTACC TCCGTTTCGA CGCTAGCCGC CTTACATGG GCGAACGTTA CAAGACCAA 3780
CATTTGAAGG TCGAGGTGCA GAAAATCGTG CCGTACATCG GACTCCTCGT CTCCGCTGAG 3840
CAGGTCGTCC TCGACCCTGT CAGGAGCGCT CTCAAGATAT TTGGGCGCTG CTACACAAGC 3900
GAACTCCTTT ACTCCAAGTA CGTGGAGGCT GTGAGAGACA TCACCAAGGG CTGGAGTGAC 3960
GCCCCGTACC ACAGCCTCCT GTGCCACATG TCAGCATGCT ACTACAATTA CGCGCCGGAG 4020
TCTGCGGCGT ACATCATCGA CGCTGTTGTT CGCTTTGGGC GCGGCGACTT CCCGTTTGAA 4080
CAACTGCGCG TGGTGCGTGC CCATGTGCAG GCACCCGACG CTTACAGCAG CACGTATCCG 4140
GCTAACGTGC GCGCATCGTG CCTTGACCAC GTCTTCGAGC CCCGCCAGGC CGCCGCCCGG 4200
GCAGGTTTCG TTGCGAC ATG TGC GAA GCC GGA AAC GCC TTC TTC ACT TAC 4250

Met Cys Glu Ala Gly Asn Ala Phe Phe Thr Tyr

1

5

10

CGC GAA AGC TGG TGT TTC TGC GAC TAC AAG CCA CGT TGC GAC TGG GAC 4298
Arg Glu Ser Trp Cys Phe Cys Asp Tyr Lys Pro Arg Cys Asp Trp Asp

15

20

25

TGC GCC CCC GGA GTC TCC ATG GGA TGC ACC TGC AGC CAA CAG CTT TTC 4346
Cys Ala Pro Gly Val Ser Met Gly Cys Thr Cys Ser Gln Gln Leu Phe

30

35

40

GGA GTT ATT GAC ACC GGA GAC CCC GTC CAC ATC ATC CTC GCC GTC ATC 4394
Gly Val Ile Asp Thr Gly Asp Pro Val His Ile Ile Leu Ala Val Ile

45

50

55

GTC TTC ATC GGA CTC CTC TAC ATC GTG TGG AAG GTC GCT CAG TGG TGG 4442
Val Phe Ile Gly Leu Leu Tyr Ile Val Trp Lys Val Ala Gln Trp Trp
60 65 70 75
AGA CAC CGC AAG GAC CAC AGA AGA CTT GAA CAG CAG AAA GCC GCC TTC 4490
Arg His Arg Lys Asp His Arg Arg Leu Glu Gln Gln Lys Ala Ala Phe
80 85 90
GCA AGA CAG GCA ATC ACG CTC GTC TGAATGTC TGGACAGAAG CGGAGAAAGG 4542
Ala Arg Gln Ala Ile Thr Leu Val
95
ACAGGCAGTT CGTAACTGC CCCCCTGCT CCGAGCCCCT CATTCTCATT TTCGAAAGA 4602
GCTCGACTGG CGACCGGGCC GACTGTCGCC GCTGCGACAT CACCTTCGGC AACCCCATCC 4662
TGCGCCACGG ACCAGGTTGC CGCGAGGACC ACGCCGGA CTGCGCCTTT CCTGGGTTCC 4722
CAGTCTGCCC GTGCTGTCTC GAAGCCGTAC CGGCCCCCA CGACTGCCC GTGGAAAGAA 4782
GTCACCCCGC TCCACGCGTG GAAGGGCGTG ACCGGAGACC GACCGGAAGT CAGGGAGGAC 4842
CCGGAGACAG CGGCGGTCGT CCAGGCTCTG ATCAGCGGCC GTTATCCTCA GAAGACGAAG 4902
CTTTCCTCCG ACGCATCCAA AGGCTACTCA AGAACTAAGG GATGCTCACA ATCCACCTCT 4962
TTTCTGCCC CGAGTGC GGA TTACAGGCC CGCGACTGCC AGACAGTCCG AGTCTGCCGC 5022
GCCGCTGCAG AGATGGCGCG CTCATGTATT CACGAGCCGT TGGCTTCATC TGCCGCCAGT 5082
GCCGACTTGA AGCGCATACG CTCTACCTCG GACTCTGTTC CCGATGTAAA GATCAGCAAG 5142
AGCGCATGAA GGAACAAAAT TAGTTTCCTT GTTCGTAAAC AAGGTGGTCC CTCCCATTGA 5202
GGTAAAGACT CTGGTGAGTC CTCAACGTTA CTCGTTGAGT CTGCTGCGGT TCGATTCCAT 5262
TCCAAGCAG CAAAGGGTGC GCAACTAGTA CGGCGCCCCC TGGGATACCA 5312

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Cys Glu Ala Gly Asn Ala Phe Phe Thr Tyr Arg Glu Ser Trp Cys
1 5 10 15
Phe Cys Asp Tyr Lys Pro Arg Cys Asp Trp Asp Cys Ala Pro Gly Val
20 25 30
Ser Met Gly Cys Thr Cys Ser Gln Gln Leu Phe Gly Val Ile Asp Thr
35 40 45
Gly Asp Pro Val His Ile Ile Leu Ala Val Ile Val Phe Ile Gly Leu
50 55 60
Leu Tyr Ile Val Trp Lys Val Ala Gln Trp Trp Arg His Arg Lys Asp
65 70 75 80
His Arg Arg Leu Glu Gln Gln Lys Ala Ala Phe Ala Arg Gln Ala Ile
85 90 95
Thr Leu Val

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4518..4937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTTCTGCCTC	CCCCGGACGG	TAAATATAGG	GGAACAATGT	ACGCGAAAGC	GACAGACGTG	60
GCGCGTGTCT	ACGCCGCGGC	AGATGTCGCC	TACGCGAACG	TACTGCAGCA	GAGAGCAGTC	120
AAGTTGGACT	TCGCCCCGCC	ACTGAAGGCA	CTAGAAACCC	TCCACAGACT	GTACTATCCG	180
CTGCGCTTCA	AAGGGGGCAC	TTTACCCCCG	ACACAACACC	CGATCCTGGC	CGGGCACCAA	240
CGTGTGCGAG	AAGAGGTTCT	GCACAATTTT	GCCAGGGGAC	GTAGCACAGT	GCTCGAGATA	300
GGGCCGTCTC	TGCACAGCGC	ACTTAAGCTA	CATGGGGCAC	CGAACGCCCC	CGTCGCAGAC	360
TATCACGGGT	GCACCAAGTA	CGGCACCCGC	GACGGCTCGC	GACACATTAC	GGCCTTAGAG	420
TCTAGATCCG	TCGCCACAGG	CCGGCCCCGAG	TTCAAGGCCG	ACGCCTCACT	GCTCGCCAAC	480
GGCATTGCCT	CCCGCACCTT	CTGCGTCGAC	GGAGTCGGCT	CTTGCGCGTT	CAAATCGCGC	540
GTTGGAATTG	CCAATCACTC	CCTCTATGAC	GTGACCCTAG	AGGAGCTGGC	CAATGCGTTT	600
GAGAACCACG	GACTTCACAT	GGTCCGCGCG	TTCATGCACA	TGCCAGAAGA	GCTGCTCTAC	660
ATGGACAACG	TGGTTAATGC	CGAGCTCGGC	TACCGCTTCC	ACGTTATTGA	AGAGCCTATG	720
GCTGTGAAGG	ACTGCGCATT	CCAGGGGGGG	GACCTCCGTC	TCCACTTCCC	TGAGTTGGAC	780
TTCATCAACG	AGAGCCAAGA	GCGGCGCATC	GAGAGGCTGG	CCGCCCCGCG	CTCCTACTCC	840
AGACGCGCCG	TCATTTTCTC	CGGCGACGAC	GACTGGGGTG	ATGCGTACTT	ACACGACTTC	900
CACACATGGC	TCGCCTACCT	ACTGGTGAGG	AACTACCCCA	CTCCGTTTGG	TTTCTCACTC	960
CATATAGAAG	TCCAGAGGCG	CCACGGCTCC	AGCATTGAGC	TGCGCATCAC	TCGCGCGCCA	1020
CCTGGAGAAC	GATCTCTGGC	CGTCGTCCCA	AGGAGCTCCC	AAGGCCCTCT	CAGAATCCCA	1080
AACATCTTTT	ATTACGCGCA	CGCGTCGGGC	ACTGAGCATA	AGACCATCCT	TACGTACAG	1140
CACAAAGTCA	ACATGCTGCT	CAATTTTATG	CAAACGCGTC	CTGAGAAGGA	ACTAGTCGAC	1200
ATGACCGTCT	TGATGTCGTT	CGCGCGCGCT	AGGCTGCGCG	CGATCGTGGT	CGCCTCAGAA	1260
GTCACCGAGA	GCTCCTGGAA	CATCTCACCG	GCTGACCTGG	TCCGCACTGT	CGTGTCTCTT	1320
TACGTCTCTC	ACATCATCGA	GCGCCGAAGG	GCTGCGGTCT	CTGTCAAGAC	CGCCAAGGAC	1380
GACGTCTTTG	GAGAGACTTC	GTTCTGGGAG	AGTCTCAAGC	ACGTCTTGGG	CTCCTGTTGC	1440
GGTCTGCGCA	ACCTCAAAGG	CACCGACGTC	GTCTTTACTA	AGCGCGTCGT	CGATAAGTAC	1500
CGAGTCCACT	CGCTCGGAGA	CATAATCTGC	GACGTCCGCC	TGTCCCCTGA	ACAGGTCGGC	1560
TTCTTGCCGT	CCCGCGTACC	ACCTGCCCCG	GTCTTTTACG	ACAGGGAAGA	GCTTGAGGTC	1620
CTTCGCGAAG	CTGGCTGCTA	CAACGAACGT	CCGGTACCTT	CCACTCCTCC	TGTGGAGGAG	1680
CCCCAAGGTT	TCGACGCCGA	CTTGTGGCAC	GCGACCGCGG	CCTCACTCCC	CGAGTACCGC	1740
GCCACCTTGC	AGGCAGGTCT	CAACACCGAC	GTCAAGCAGC	TCAAGATCAC	CCTCGAGAAC	1800
GCCCTCAAGA	CCATCGACGG	GCTCACCCCT	TCCCCAGTCA	GAGGCCTCGA	GATGTACGAG	1860
GGCCCGCCAG	GCAGCGGCAA	GACGGGCACC	CTCATCGCCG	CCCTTGAGGC	CGCGGGCGGT	1920
AAAGCACTTT	ACGTGGCACC	CACCAGAGAA	CTGAGAGAGG	CTATGGACCG	GCGGATCAAA	1980
CCGCCGTCTG	CCTCGGCTAC	GCAACATGTC	GCCCTTGCGA	TTCTCCGTCT	TGCCACCGCC	2040
GAGGGCGCCC	CTTTCGCTAC	CTGGGTTATC	GACGAGTGCT	TCATGTTCCC	GCTCGTGTAC	2100
GTCGCGATCG	TGCACGCCCT	GTCCCCGAGC	TCACGAATAG	TCCTTGTAGG	GGACGTCCAC	2160
CAAATCGGGT	TTATAGACTT	CCAAGGCACA	AGCGCGAACA	TGCCGCTCGT	TCGCGACGTC	2220
GTTAAGCAGT	GCCGTCGGCG	CACCTTCAAC	CAAACCAAGC	GCTGTCCGGC	CGACGTCGTT	2280
GCCACCACGT	TTTTCCAGAG	CTTGTACCCC	GGGTGCACAA	CCACCTCAGG	GTGCGTCGCA	2340
TCCATCAGCC	ACGTCGCCCC	AGACTACCGC	AACAGCCAGG	CGCAAACGCT	CTGCTTCACG	2400
CAGGAGGAAA	AGTCGCGCCA	CGGGGCTGAG	GGCGCGATGA	CTGTGCACGA	AGCGCAGGGA	2460
CGCACTTTTG	CGTCTGTCAT	TCTGCATTAC	AACGGCTCCA	CAGCAGAGCA	GAAGCTCCTC	2520
GCTGAGAAGT	CGCACCTTCT	AGTCGGCATC	ACGCGCCACA	CCAACCACCT	GTACATCCGC	2580
GACCCGACAG	GTGACATTGA	GAGACAACCT	AACCATAGCG	CGAAAGCCGA	GGTGTTTACA	2640
GACATCCCTG	CACCCCTGGA	GATCACGACT	GTCAAACCGA	GTGAAGAGGT	GCAGCGCAAC	2700
GAAGTGATGG	CAACGATACC	CCCGCAGAGT	GCCACGCCGC	ACGGAGCAAT	CCATCTGCTC	2760
CGCAAGAACT	TCGGGGACCA	ACCCGACTGT	GGCTGTGTCT	CTTTGGCGAA	GACCGGCTAC	2820
GAGGTGTTTG	GCGGTCGTGC	CAAAATCAAC	GTAGAGCTTG	CCGAACCCGA	CGCGACCCCG	2880
AAGCCGCATA	GGGCGTTCCA	GGAAGGGGTA	CAGTGGGTCA	AGGTACACAA	CGCGTCTAAC	2940
AAACACCAAG	CGTCCAGAG	GCTGTTGTCT	CGCTACACCA	AGCGAAGCGC	TGACCTGCCG	3000
CTACACGAAG	CTAAGGAGGA	CGTCAAACGC	ATGCTAAACT	CGCTTGACCG	ACATTGGGAC	3060
TGGACTGTCA	CTGAAGACGC	CCGTGACCGA	GCTGTCTTCG	AGACCCAGCT	CAAGTTCACC	3120
CAACGCGGCG	GCACCGTCGA	AGACCTGCTG	GAGCCAGACG	ACCCCTACAT	CCGTGACATA	3180
GACTTCCTTA	TGAAGACTCA	GCAGAAAGTG	TCGCCCAAGC	CGATCAATAC	GGGCAAGGTC	3240
GGGCAGGGGA	TCGCCGCTCA	CTCAAAGTCT	CTCAACTTCG	TCCTCGCCGC	TTGGATACGC	3300
ATACTCGAGG	AGATACTCCG	TACCGGGGAG	CGCACGGTCC	GGTACAGCAA	CGGTCTCCCC	3360

GACGAAGAAG AGGCCATGCT GCTCGAAGCG AAGATCAATC AAGTCCCACA CGCCACGTTC 3420
 GTCTCGGCGG ACTGGACCGA GTTTGACACC GCCACAATA ACACGAGTGA GCTGCTCTTC 3480
 GCCGCCCTTT TAGAGCGCAT CGGCACGCCT GCAGCTGCCG TTAATCTATT CAGAGAACGG 3540
 TGTGGGAAAC GCACCTTGCG AGCGAAGGGT CTAGGCTCCG TTGAAGTCGA CGGTCTGCTC 3600
 GACTCCGGCG CAGCTTGGAC GCCTTGCCGC AACACCATCT TCTCTGCCGC CGTCATGCTC 3660
 ACGCTCTTCC GCGGCGTCAA GTTCGCAGCT TTCAAAGGCG ACGACTCGCT CCTCTGTGGT 3720
 AGCCATTACC TCCGTTTCGA CGCTAGCCGC CTTACATGG GCGAACGTTA CAAGACCAAA 3780
 CATTGAAGG TCGAGGTGCA GAAAATCGTG CCGTACATCG GACTCCTCGT CTCCGCTGAG 3840
 CAGGTCGTCC TCGACCCTGT CAGGAGCGCT CTCAAGATAT TTGGGCGCTG CTACACAAGC 3900
 GAACTCCTTT ACTCCAAGTA CGTGGAGGCT GTGAGAGACA TCACCAAGGG CTGGAGTGAC 3960
 GCCCGCTACC ACAGCCTCCT GTGCCACATG TCAGCATGCT ACTACAATTA CGCGCCGGAG 4020
 TCTGCGGCGT ACATCATCGA CGCTGTTGTT CGCTTTGGGC GCGGCGACTT CCCGTTTGAA 4080
 CAACTGCGCG TGGTGCGTGC CCATGTGCAG GCACCCGACG CTTACAGCAG CACGTATCCG 4140
 GCTAACGTGC GCGCATCGTG CCTTGACCAC GTCTTCGAGC CCCGCCAGGC CGCCGCCCCG 4200
 GCAGGTTTCG TTGCGACATG TGCGAAGCCG GAAACGCCTT CTTCACTTAC CGCGAAAGCT 4260
 GGTGTTTCTG CGACTACAAG CCACGTTGCG ACTGGGACTG CGCCCCCGGA GTCTCCATGG 4320
 GATGCACCTG CAGCCAACAG CTTTTCGGAG TTATTGACAC CGGAGACCCC GTCCACATCA 4380
 TCCTCGCCGT CATCGTCTTC ATCGGACTCC TCTACATCGT GTGGAAGGTC GCTCAGTGGT 4440
 GGAGACACCG CAAGGACCAC AGAAGACTTG AACAGCAGAA AGCCGCCTTC GCAAGACAGG 4500
 CAATCACGCT CGTCTGA ATG TCT GGA CAG AAG CGG AGA AAG GAC AGG CAG 4550

Met Ser Gly Gln Lys Arg Arg Lys Asp Arg Gln

1 5 10
 TTC GTT AAC TGC CCC CAC TGC TCC GAG CCC CTC ATT CTC ATT TTC GGA 4598
 Phe Val Asn Cys Pro His Cys Ser Glu Pro Leu Ile Leu Ile Phe Gly
 15 20 25
 AAG AGC TCG ACT GGC GAC CGG GCC GAC TGT CGC CGC TGC GAC ATC ACC 4646
 Lys Ser Ser Thr Gly Asp Arg Ala Asp Cys Arg Arg Cys Asp Ile Thr
 30 35 40
 TTC GGC AAC CCC ATC CTG CGC CAC GGA CCA GGT TGC CGC GAG GAC CAC 4694
 Phe Gly Asn Pro Ile Leu Arg His Gly Pro Gly Cys Arg Glu Asp His
 45 50 55
 GCC GGA CTT TGC GCC TTT CCT GGG TTC CCA GTC TGC CCG TGC TGT CTC 4742
 Ala Gly Leu Cys Ala Phe Pro Gly Phe Pro Val Cys Pro Cys Cys Leu
 60 65 70 75
 GAA GCC GTA CCG GCC CAC GAC TGC CCG TTG GAA AGA AGT CAC CCC 4790
 Glu Ala Val Pro Ala Pro His Asp Cys Pro Leu Glu Arg Ser His Pro
 80 85 90
 GCT CCA CGC GTG GAA GGG CGT GAC CGG AGA CCG ACC GGA AGT CAG GGA 4838
 Ala Pro Arg Val Glu Gly Arg Asp Arg Arg Pro Thr Gly Ser Gln Gly
 95 100 105
 GGA CCC GGA GAC AGC GGC GGT CGT CCA GGC TCT GAT CAG CGG CCG TTA 4886
 Gly Pro Gly Asp Ser Gly Gly Arg Pro Gly Ser Asp Gln Arg Pro Leu
 110 115 120
 TCC TCA GAA GAC GAA GCT TTC CTC CGA CGC ATC CAA AGG CTA CTC AAG 4934
 Ser Ser Glu Asp Glu Ala Phe Leu Arg Arg Ile Gln Arg Leu Leu Lys
 125 130 135
 AAC TAAGGGATGC TCACAATCCA CCTCTTTTCC TGCCCCGAGT GCGGATTACC 4987
 Asn
 140
 AGGCCCCGCGA CTGCCAGACA GTCCGAGTCT GCCGCGCCGC TGCAGAGATG GCGCGCTCAT 5047
 GTATTACAGA GCCGTTGGCT TCATCTGCCG CCAGTGCCGA CTTGAAGCGC ATACGCTCTA 5107
 CCTCGGACTC TGTTCCCGAT GTAAAGATCA GCAAGAGCGC ATGAAGGAAC AAAATTAGTT 5167
 TCCTTGTTTCG TAAACAAGGT GGTCCCTCCC ATTGAGGTAA AGACTCTGGT GAGTCCTCAA 5227
 CGTTACTCGT TGAGTCTGCT GCGGTTTCGAT TCCATTCCCA AGCAGCAAAG GGTGCGCAAC 5287
 TAGTACGGCG CCCCCTGGGA TACCA 5312

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Ser Gly Gln Lys Arg Arg Lys Asp Arg Gln Phe Val Asn Cys Pro
1 5 10 15
His Cys Ser Glu Pro Leu Ile Leu Ile Phe Gly Lys Ser Ser Thr Gly
20 25 30
Asp Arg Ala Asp Cys Arg Arg Cys Asp Ile Thr Phe Gly Asn Pro Ile
35 40 45
Leu Arg His Gly Pro Gly Cys Arg Glu Asp His Ala Gly Leu Cys Ala
50 55 60
Phe Pro Gly Phe Pro Val Cys Pro Cys Cys Leu Glu Ala Val Pro Ala
65 70 75 80
Pro His Asp Cys Pro Leu Glu Arg Ser His Pro Ala Pro Arg Val Glu
85 90 95
Gly Arg Asp Arg Arg Pro Thr Gly Ser Gln Gly Gly Pro Gly Asp Ser
100 105 110
Gly Gly Arg Pro Gly Ser Asp Gln Arg Pro Leu Ser Ser Glu Asp Glu
115 120 125
Ala Phe Leu Arg Arg Ile Gln Arg Leu Leu Lys Asn
130 135 140

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 4944..5162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTTCTGCCTC CCCCGGACGG TAAATATAGG GGAACAATGT ACGCGAAAGC GACAGACGTG 60
GCGCGTGTCT ACGCCGCGGC AGATGTCGCC TACGCGAACG TACTGCAGCA GAGAGCAGTC 120
AAGTTGGACT TCGCCCCGCC ACTGAAGGCA CTAGAAACCC TCCACAGACT GTACTATCCG 180
CTGCGCTTCA AAGGGGGCAC TTTACCCCGG ACACAACACC CGATCCTGGC CGGGCACCAA 240
CGTGTGCGAG AAGAGGTTCT GCACAATTTT GCCAGGGGAC GTAGCACAGT GCTCGAGATA 300
GGGCCGTCTC TGCACAGCGC ACTTAAGCTA CATGGGGCAC CGAACGCCCC CGTCGCAGAC 360
TATCACGGGT GCACCAAGTA CGGCACCCGC GACGGCTCGC GACACATTAC GGCCTTAGAG 420
TCTAGATCCG TCGCCACAGG CCGGCCGAG TTCAAGGCCG ACGCCTCACT GCTCGCCAAC 480
GGCATTGCCT CCCGCACCTT CTGCGTCGAC GGAGTCGGCT CTTGCGCGTT CAAATCGCGC 540
GTTGGAATTG CCAATCACTC CCTCTATGAC GTGACCCTAG AGGAGCTGGC CAATGCGTTT 600
GAGAACCACG GACTTCACAT GGTCCGCGCG TTCATGCACA TGCCAGAAGA GCTGCTCTAC 660
ATGGACAACG TGGTTAATGC CGAGCTCGGC TACCGCTTCC ACGTTATTGA AGAGCCTATG 720
GCTGTGAAGG ACTGCGCATT CCAGGGGGG GACCTCCGTC TCCACTTCCC TGAGTTGGAC 780
TTCATCAACG AGAGCCAAGA GCGGCGCATC GAGAGGCTGG CCGCCGCGCG CTCCTACTCC 840
AGACGCGCCG TCATTTTCTC CGGCGACGAC GACTGGGGTG ATGCGTACTT ACACGACTTC 900
CACACATGGC TCGCCTACCT ACTGGTGAGG AACTACCCCA CTCCGTTTGG TTTCTCACTC 960
CATATAGAAG TCCAGAGGCG CCACGGCTCC AGCATTGAGC TGCGCATCAC TCGCGGCCA 1020
CCTGGAGACC GCATGCTGGC CGTCGTCCCA AGGACGTCCC AAGGCCTCTG CAGAATCCCA 1080
AACATCTTTT ATTACGCCGA CGCGTCGGGC ACTGAGCATA AGACCATCCT TACGTCACAG 1140

CACAAAGTCA	ACATGCTGCT	CAATTTTATG	CAAACGCGTC	CTGAGAAGGA	ACTAGTCGAC	1200
ATGACCGTCT	TGATGTCGTT	CGCGCGCGCT	AGGCTGCGCG	CGATCGTGGT	CGCCTCAGAA	1260
GTCACCGAGA	GCTCCTGGAA	CATCTCACCG	GCTGACCTGG	TCCGCACTGT	CGTGTCTCTT	1320
TACGTCTCTC	ACATCATCGA	GCGCCGAAGG	GCTGCGGTTCG	CTGTCAAGAC	CGCCAAGGAC	1380
GACGTCTTTG	GAGAGACTTC	GTTCTGGGAG	AGTCTCAAGC	ACGTCTTGGG	CTCCTGTTGC	1440
GGTCTGCGCA	ACCTCAAAGG	CACCGACGTC	GTCTTTACTA	AGCGCGTCGT	CGATAAGTAC	1500
CGAGTCCACT	CGCTCGGAGA	CATAATCTGC	GACGTCCGCC	TGTCCCCTGA	ACAGGTCGGC	1560
TTCTTGCCGT	CCCGCGTACC	ACCTGCCCGC	GTCTTTTACG	ACAGGGAAGA	GCTTGAGGTC	1620
CTTCGCGAAG	CTGGCTGCTA	CAACGAACGT	CCGGTACCTT	CCACTCCTCC	TGTGGAGGAG	1680
CCCCAAGGTT	TCGACGCCGA	CTTGTGGCAC	GCGACCGCGG	CCTCACTCCC	CGAGTACCGC	1740
GCCACCTTGC	AGGCAGGTCT	CAACACCGAC	GTCAAGCAGC	TCAAGATCAC	CCTCGAGAAC	1800
GCCCTCAAGA	CCATCGACGG	GCTCACCCCTC	TCCCCAGTCA	GAGGCCTCGA	GATGTACGAG	1860
GGCCCCGCCAG	GCAGCGGCAA	GACGGGCACC	CTCATCGCCG	CCCTTGAGGC	CGCGGGCGGT	1920
AAAGCACTTT	ACGTGGCACC	CACCAGAGAA	CTGAGAGAGG	CTATGGACCG	GCGGATCAAA	1980
CCGCCGTCCG	CCTCGGCTAC	GCAACATGTC	GCCCTTGCGA	TTCTCCGTCG	TGCCACCGCC	2040
GAGGGCGCCC	CTTTCGCTAC	CGTGTTTATC	GACGAGTGCT	TCATGTTCCC	GCTCGTGTAC	2100
GTGCGGATCG	TGCACGCCTT	GTCCCCGAGC	TCACGAATAG	TCCTTGTAGG	GGACGTCCAC	2160
CAAAATCGGGT	TTATAGACTT	CCAAGGCACA	AGCGCGAACA	TGCCGCTCGT	TCGCGACGTC	2220
GTTAAGCAGT	GCCGTCGGCG	CACTTTCAAC	CAAAACAAGC	GCTGTCCGGC	CGACGTCGTT	2280
GCCACCACGT	TTTTCCAGAG	CTTGTACCCC	GGGTGCACAA	CCACCTCAGG	GTGCGTCGCA	2340
TCCATCAGCC	ACGTGCGCCC	AGACTACCGC	AACAGCCAGG	CGCAAACGCT	CTGCTTCACG	2400
CAGGAGGAAA	AGTCGCGCCA	CGGGGCTGAG	GGCGCGATGA	CTGTGCACGA	AGCGCAGGGA	2460
CGCACTTTTG	CGTCTGTCAT	TCTGCATTAC	AACGGCTCCA	CAGCAGAGCA	GAAGCTCCTC	2520
GCTGAGAAGT	CGCACCTTCT	AGTCGGCATC	ACGCGCCACA	CCAACCACCT	GTACATCCGC	2580
GACCCGACAG	GTGACATTGA	GAGACAACCT	AACCATAGCG	CGAAAGCCGA	GGTGTTTACA	2640
GACATCCCTG	CACCCCTGGA	GATCACGACT	GTCAAACCGA	GTGAAGAGGT	GCAGCGCAAC	2700
GAAGTGATGG	CAACGATACC	CCCGCAGAGT	GCCACGCCGC	ACGGAGCAAT	CCATCTGCTC	2760
CGCAAGAACT	TCGGGGACCA	ACCCGACTGT	GGCTGTGTCTG	CTTTGGCGAA	GACCGGCTAC	2820
GAGGTGTTTG	GCGGTGCTGC	CAAAATCAAC	GTAGAGCTTG	CCGAACCCGA	CGCGACCCCG	2880
AAGCCGCATA	GGGCGTTCCA	GGAAGGGGTA	CAGTGGGTCA	AGGTCACCAA	CGCGTCTAAC	2940
AAACACCAGG	CGCTCCAGAC	GCTGTTGTCC	CGCTACACCA	AGCGAAGCGC	TGACCTGCCG	3000
CTACACGAAG	CTAAGGAGGA	CGTCAAACGC	ATGCTAAACT	CGCTTGACCG	ACATTGGGAC	3060
TGGACTGTCA	CTGAAGACGC	CCGTGACCGA	GCTGTCTTCG	AGACCCAGCT	CAAGTTCACC	3120
CAACGCGGCG	GCACCGTCA	AGACCTGCTG	GAGCCAGACG	ACCCCTACAT	CCGTGACATA	3180
GACTTCCTTA	TGAAGACTGA	GCAGAAAGTG	TGCCCCAAGC	CGATCAATAC	GGGCAAGGTC	3240
GGGCAGGGGA	TCGCCGCTCA	CTCAAAGTCT	CTCAACTTCG	TCCTCGCCGC	TTGGATACGC	3300
ATACTCGAGG	AGATACTCCG	TACCGGGAGC	CGCACGGTCC	GGTACAGCAA	CGGTCTCCCC	3360
GACGAAGAAG	AGGCCATGCT	GCTCGAAGCG	AAGATCAATC	AAGTCCCACA	CGCCACGTTC	3420
GTCTCGGCGG	ACTGGACCGA	GTTTGACACC	GCCCACAATA	ACACGAGTGA	GCTGCTCTTC	3480
GCCGCCCTTT	TAGAGCGCAT	CGGCACGCCT	GCAGCTGCCG	TTAATCTATT	CAGAGAACGG	3540
TGTGGGAAAC	GCACCTTGCG	AGCGAAGGGT	CTAGGCTCCG	TTGAAGTCGA	CGGTCTGCTC	3600
GACTCCGGCG	CAGCTTGGAC	GCCTTGCCGC	AACACCATCT	TCTCTGCCGC	CGTCATGCTC	3660
ACGCTCTTCC	GCGGCGTCAA	GTTTCGAGCT	TTCAAAGGCG	ACGACTCGCT	CCTCTGTGGT	3720
AGCCATTACC	TCCGTTTTCGA	CGCTAGCCGC	CTTCACATGG	GCGAACGTTA	CAAGACCAAA	3780
CATTTGAAGG	TCGAGGTGCA	GAAAATCGTG	CCGTACATCG	GACTCCTCGT	CTCCGCTGAG	3840
CAGGTCGTCC	TCGACCCTGT	CAGGAGCGCT	CTCAAGATAT	TTGGGCGCTG	CTACACAAGC	3900
GAACTCCTTT	ACTCCAAGTA	CGTGGAGGCT	GTGAGAGACA	TCACCAAGGG	CTGGAGTGAC	3960
GCCCGCTACC	ACAGCCTCCT	GTGCCACATG	TCAGCATGCT	ACTACAATTA	CGCGCCGGAG	4020
TCTGCGGCGT	ACATCATCGA	CGCTGTTGTT	CGCTTTGGGG	GCGGCGACTT	CCCGTTTGAA	4080
CAACTGCGCG	TGGTGCCTGC	CCATGTGCAG	GCACCCCAGC	CTTACAGCAG	CACGTATCCG	4140
GCTAACGTGC	GCGCATCGTG	CCTTGACCAC	GTCTTCGAGC	CCCGCCAGGC	CGCCGCCCCG	4200
GCAGGTTTCG	TTGCGACATG	TGCGAAGCCG	GAAACGCCTT	CTTCACTTAC	CGCGAAAGCT	4260
GGTGTTCCTG	CGACTACAAG	CCACGTTGCG	ACTGGGACTG	CGCCCCCGGA	GTCTCCATGG	4320
GATGCACCTG	CAGCCAACAG	CTTTTCGGAG	TTATTGACAC	CGGAGACCCC	GTCCACATCA	4380
TCCTCGCCGT	CATCGTCTTC	ATCGGACTCC	TCTACATCGT	GTGGAAGGTC	GCTCAGTGGT	4440
GGAGACACCG	CAAGGACCAC	AGAAGACTTG	AACAGCAGAA	AGCCGCCTTC	GCAAGACAGG	4500
CAATCACGCT	CGTCTGAATG	TCTGGACAGA	AGCGGAGAAA	GGACAGGCAG	TTCGTTAACT	4560

GCCCCCACTG CTCCGAGCCC CTCATTCTCA TTTTCGGAAA GAGCTCGACT GGCGACCGGG 4620
 CCGACTGTCG CCGCTGCGAC ATCACCTTCG GCAACCCCAT CCTGCGCCAC GGACCAGGTT 4680
 GCCGCGAGGA CCACGCCGGA CTTTGCGCCT TTCCTGGGTT CCCAGTCTGC CCGTGCTGTC 4740
 TCGAAGCCGT ACCGGCCCCC CACGACTGCC CGTTGGAAAG AAGTCACCCC GCTCCACGCG 4800
 TGGAAGGGCG TGACCGGAGA CCGACCGGAA GTCAGGGAGG ACCCGGAGAC AGCGGCGGTC 4860
 GTCCAGGCTC TGATCAGCGG CCGTTATCCT CAGAAGACGA AGCTTTCCTC CGACGCATCC 4920
 AAAGGCTACT CAAGAACTAA GGG ATG CTC ACA ATC CAC CTC TTT TCC TGC 4970

Met Leu Thr Ile His Leu Phe Ser Cys

1 5
 CCC GAG TGC GGA TTA CCA GGC CCG CGA CTG CCA GAC AGT CCG AGT CTG 5018
 Pro Glu Cys Gly Leu Pro Gly Pro Arg Leu Pro Asp Ser Pro Ser Leu
 10 15 20 25
 CCG CGC CGC TGC AGA GAT GGC GCG CTC ATG TAT TCA CGA GCC GTT GGC 5066
 Pro Arg Arg Cys Arg Asp Gly Ala Leu Met Tyr Ser Arg Ala Val Gly
 30 35 40
 TTC ATC TGC CGC CAG TGC CGA CTT GAA GCG CAT ACG CTC TAC CTC GGA 5114
 Phe Ile Cys Arg Gln Cys Arg Leu Glu Ala His Thr Leu Tyr Leu Gly
 45 50 55
 CTC TGT TCC CGA TGT AAA GAT CAG CAA GAG CGC ATG AAG GAA CAA AAT 5162
 Leu Cys Ser Arg Cys Lys Asp Gln Gln Glu Arg Met Lys Glu Gln Asn
 60 65 70
 TAGTTTCCTT GTTCGTAAAC AAGGTGGTCC CTCCCATTGA GGTAAGACT CTGGTGAGTC 5222
 CTCAACGTTA CTCGTTGAGT CTGCTGCGGT TCGATTCCAT TCCAAGCAG CAAAGGGTGC 5282
 GCAACTAGTA CGGCGCCCCC TGGGATACCA 5312

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Leu Thr Ile His Leu Phe Ser Cys Pro Glu Cys Gly Leu Pro Gly
 1 5 10 15
 Pro Arg Leu Pro Asp Ser Pro Ser Leu Pro Arg Arg Cys Arg Asp Gly
 20 25 30
 Ala Leu Met Tyr Ser Arg Ala Val Gly Phe Ile Cys Arg Gln Cys Arg
 35 40 45
 Leu Glu Ala His Thr Leu Tyr Leu Gly Leu Cys Ser Arg Cys Lys Asp
 50 55 60
 Gln Gln Glu Arg Met Lys Glu Gln Asn
 65 70

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 283..753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTTTTTCTTT CTTTACCAAG TGTGGTAAAA TTAAACAAA GAAGAAAACC AGGACCGTAA 60

Cf

TGCCTCGCCG	ACGACCTGGC	CACCCGTCTC	ACAGGTGTCT	ACCCCGCCAC	TGACAACTTC	2093
GCGGCCGCCG	TTTCTGCCTT	CGCCGCGAAC	ATGCTGTCCT	CCGTGCTGAA	GTCGGAGGCA	2153
ACGTCCTCCA	TCATCAAGTC	CGTTGGCGAG	ACTGCCGTCG	GCGCGGCTCA	GTCCGGCCTC	2213
GCGAAGCTAC	CCGGACTGCT	AATGAGTGTA	CCAGGGAAGA	TTGCCGCGCG	TGTCCGCGCG	2273
CGCCGAGCGC	GCCGCCGCGC	CGCTCGTGCC	AATTAGTTTG	CTCGCTCCTG	TTTCGCCGTT	2333
TCGTAAAACG	GCGTGGTCCC	GCACATTACG	CGTACCCTAA	AGACTCTGGT	GAGTCCCCGT	2393
CGTTACACGA	CGGGTCTGCC	GCGGTTTCAT	TCCATTCCCA	AGCGGCAAGA	AGGACGTAGT	2453
TAGCTCTGCG	TCCCTCGGGA	TACCA				2478

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Ser Glu His Thr Ile Ala His Ser Ile Thr Leu Pro Pro Gly Tyr
1 5 10 15
Thr Leu Ala Leu Ile Pro Pro Glu Pro Glu Ala Gly Trp Glu Met Leu
20 25 30
Glu Trp Arg His Ser Asp Leu Thr Thr Val Ala Glu Pro Val Thr Phe
35 40 45
Gly Ser Ala Pro Thr Pro Ser Pro Ser Met Val Glu Glu Thr Asn Gly
50 55 60
Val Gly Pro Glu Gly Lys Phe Leu Pro Leu Thr Ile Ser Pro Leu Leu
65 70 75 80
His Lys Thr Ser Arg Lys Ala Leu Thr Pro Thr Pro Ser Leu Ser Pro
85 90 95
Leu Thr Ser Leu Ala Cys Pro Asn Ser Gly Ile Gly Pro Arg Glu Arg
100 105 110
Ser Thr Ser Thr Pro Ile Pro Ser Ala Gly Thr Ser Ser Thr Leu Thr
115 120 125
Gln Arg Val Leu Gln Ser Leu Arg Ala Pro Ser Ala Ser Thr Arg Arg
130 135 140
Ser Leu Thr Ala Ser Ser Ser Ser Pro Ser Thr Gln Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 366..2306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTTTTTCTTT	CTTTACCAAG	TGTGGTAAAA	TTTAAACAAA	GAAGAAAACC	AGGACCGTAA	60
CCCGGCCCTT	ACACACCTCG	AGTCCGTGAC	CACCGGATTA	TACGTCGCCC	ACCACACGGC	120
GCCTTTTCCG	ACCACTCTCG	AGAGTCGTTG	GGAGTTTCGT	CCGTGACCAC	CCGGTTGGCA	180
GTCGACAGAC	GCTTCCGGAC	CACTAGAACC	TCCTCGAGCG	ACGCACACAC	AGCACACACA	240
CCGCCTTAGC	TGCACCTACG	GCAGCGTTGA	TAGCGCGGAT	TTATGAGCGA	GCACACCATC	300
GGCCACTCCA	TCACATTACC	ACCCGGTTAC	ACCCTTGCCC	TAATACCCCC	TGAACCTGAA	360

GCAGG ATG GGA GAT GCT GGA GTG GCG TCA CAG CGA CCT CAC AAC CGT	407
Met Gly Asp Ala Gly Val Ala Ser Gln Arg Pro His Asn Arg	
1 5 10	
CGC GGA ACC CGT AAC GTT CGG GTC AGC GCC AAC ACC GTC ACC GTC AAT	455
Arg Gly Thr Arg Asn Val Arg Val Ser Ala Asn Thr Val Thr Val Asn	
15 20 25 30	
GGT AGA AGA AAC CAA CGG CGT CGG ACC GGA AGG CAA GTT TCT CCC CCT	503
Gly Arg Arg Asn Gln Arg Arg Arg Thr Gly Arg Gln Val Ser Pro Pro	
35 40 45	
GAC AAT TTC ACC GCT GCT GCA CAA GAC CTC GCG CAA AGC CTT GAC GCC	551
Asp Asn Phe Thr Ala Ala Ala Gln Asp Leu Ala Gln Ser Leu Asp Ala	
50 55 60	
AAC ACC GTC ACT TTC CCC GCT AAC ATC TCT AGC ATG CCC GAA TTC CGG	599
Asn Thr Val Thr Phe Pro Ala Asn Ile Ser Ser Met Pro Glu Phe Arg	
65 70 75	
AAT TGG GCC AAG GGA AAG ATC GAC CTC GAC TCC GAT TCC ATC GGC TGG	647
Asn Trp Ala Lys Gly Lys Ile Asp Leu Asp Ser Asp Ser Ile Gly Trp	
80 85 90	
TAC TTC AAG TAC CTT GAC CCA GCG GGT GCT ACA GAG TCT GCG CGC GCC	695
Tyr Phe Lys Tyr Leu Asp Pro Ala Gly Ala Thr Glu Ser Ala Arg Ala	
95 100 105 110	
GTC GGC GAG TAC TCG AAG ATC CCT GAC GGC CTC GTC AAG TTC TCC GTC	743
Val Gly Glu Tyr Ser Lys Ile Pro Asp Gly Leu Val Lys Phe Ser Val	
115 120 125	
GAC GCA GAG ATA AGA GAG ATC TAT AAC GAG GAG TGC CCC GTC GTC ACT	791
Asp Ala Glu Ile Arg Glu Ile Tyr Asn Glu Glu Cys Pro Val Val Thr	
130 135 140	
GAC GTG TCC GTC CCC CTC GAC GGC CGC CAG TGG AGC CTC TCG ATT TTC	839
Asp Val Ser Val Pro Leu Asp Gly Arg Gln Trp Ser Leu Ser Ile Phe	
145 150 155	
TCC TTT CCG ATG TTC AGA ACC GCC TAC GTC GCC GTA GCG AAC GTC GAG	887
Ser Phe Pro Met Phe Arg Thr Ala Tyr Val Ala Val Ala Asn Val Glu	
160 165 170	
AAC AAG GAG ATG TCG CTC GAC GTT GTC AAC GAC CTC ATC GAG TGG CTC	935
Asn Lys Glu Met Ser Leu Asp Val Val Asn Asp Leu Ile Glu Trp Leu	
175 180 185 190	
AAC AAT CTC GCC GAC TGG CGT TAT GTC GTT GAC TCT GAA CAG TGG ATT	983
Asn Asn Leu Ala Asp Trp Arg Tyr Val Val Asp Ser Glu Gln Trp Ile	
195 200 205	
AAC TTC ACC AAT GAC ACC ACG TAC TAC GTC CGC ATC CGC GTT CTA CGT	1031
Asn Phe Thr Asn Asp Thr Thr Tyr Tyr Val Arg Ile Arg Val Leu Arg	
210 215 220	
CCA ACC TAC GAC GTT CCA GAC CCC ACA GAG GGC CTT GTT CGC ACA GTC	1079
Pro Thr Tyr Asp Val Pro Asp Pro Thr Glu Gly Leu Val Arg Thr Val	
225 230 235	
TCA GAC TAC CGC CTC ACT TAT AAG GCG ATA ACA TGT GAA GCC AAC ATG	1127
Ser Asp Tyr Arg Leu Thr Tyr Lys Ala Ile Thr Cys Glu Ala Asn Met	
240 245 250	
CCA ACA CTC GTC GAC CAA GGC TTT TGG ATC GGC GGC CAG TAC GCT CTC	1175
Pro Thr Leu Val Asp Gln Gly Phe Trp Ile Gly Gly Gln Tyr Ala Leu	
255 260 265 270	
ACC CCG ACT AGC CTA CCG CAG TAC GAC GTC AGC GAG GCC TAC GCT CTG	1223
Thr Pro Thr Ser Leu Pro Gln Tyr Asp Val Ser Glu Ala Tyr Ala Leu	
275 280 285	
CAC ACT TTG ACC TTC GCC AGA CCA TCC AGC GCC GCT GCA CTC GCG TTT	1271
His Thr Leu Thr Phe Ala Arg Pro Ser Ser Ala Ala Ala Leu Ala Phe	
290 295 300	

GTG TGG GCA GGT TTG CCA CAG GGT GGC ACT GCG CCT GCA GGC ACT CCA 1319
 Val Trp Ala Gly Leu Pro Gln Gly Gly Thr Ala Pro Ala Gly Thr Pro
 305 310 315
 GCC TGG GAG CAG GCA TCC TCG GGT GGC TAC CTC ACC TGG CGC CAC AAC 1367
 Ala Trp Glu Gln Ala Ser Ser Gly Gly Tyr Leu Thr Trp Arg His Asn
 320 325 330
 GGT ACT ACT TTC CCA GCT GGC TCC GTT AGC TAC GTT CTC CCT GAG GGT 1415
 Gly Thr Thr Phe Pro Ala Gly Ser Val Ser Tyr Val Leu Pro Glu Gly
 335 340 345 350
 TTC GCC CTT GAG CGC TAC GAC CCG AAC GAC GGC TCT TGG ACC GAC TTC 1463
 Phe Ala Leu Glu Arg Tyr Asp Pro Asn Asp Gly Ser Trp Thr Asp Phe
 355 360 365
 GCT TCC GCA GGA GAC ACC GTC ACT TTC CGG CAG GTC GCC GTC GAC GAG 1511
 Ala Ser Ala Gly Asp Thr Val Thr Phe Arg Gln Val Ala Val Asp Glu
 370 375 380
 GTC GTT GTG ACC AAC AAC CCC GCC GGC GGC GGC AGC GCC CCC ACC TTC 1559
 Val Val Val Thr Asn Asn Pro Ala Gly Gly Gly Ser Ala Pro Thr Phe
 385 390 395
 ACC GTG AGA GTG CCC CCT TCA AAC GCT TAC ACC AAC ACC GTG TTT AGG 1607
 Thr Val Arg Val Pro Pro Ser Asn Ala Tyr Thr Asn Thr Val Phe Arg
 400 405 410
 AAC ACG CTC TTA GAG ACT CGA CCC TCC TCT CGT AGG CTC GAA CTC CCT 1655
 Asn Thr Leu Leu Glu Thr Arg Pro Ser Ser Arg Arg Leu Glu Leu Pro
 415 420 425 430
 ATG CCA CCT GCT GAC TTT GGA CAG ACG GTC GCC AAC AAC CCG AAG ATC 1703
 Met Pro Pro Ala Asp Phe Gly Gln Thr Val Ala Asn Asn Pro Lys Ile
 435 440 445
 GAG CAG TCG CTT CTT AAA GAA ACA CTT GGC TGC TAT TTG GTC CAC TCC 1751
 Glu Gln Ser Leu Leu Lys Glu Thr Leu Gly Cys Tyr Leu Val His Ser
 450 455 460
 AAA ATG CGA AAC CCC GTT TTC CAG CTC ACG CCA GCC AGC TCC TTT GGC 1799
 Lys Met Arg Asn Pro Val Phe Gln Leu Thr Pro Ala Ser Ser Phe Gly
 465 470 475
 GCC GTT TCC TTC AAC AAT CCG GGT TAT GAG CGC ACA CGC GAC CTC CCG 1847
 Ala Val Ser Phe Asn Asn Pro Gly Tyr Glu Arg Thr Arg Asp Leu Pro
 480 485 490
 GAC TAC ACT GGC ATC CGT GAC TCA TTC GAC CAG AAC ATG TCC ACC GCT 1895
 Asp Tyr Thr Gly Ile Arg Asp Ser Phe Asp Gln Asn Met Ser Thr Ala
 495 500 505 510
 GTG GCC CAC TTC CGC TCA CTC TCC CAC TCC TGC AGT ATC GTC ACT AAG 1943
 Val Ala His Phe Arg Ser Leu Ser His Ser Cys Ser Ile Val Thr Lys
 515 520 525
 ACC TAC CAG GGT TGG GAA GGC GTC ACG AAC GTC AAC ACG CCT TTC GGC 1991
 Thr Tyr Gln Gly Trp Glu Gly Val Thr Asn Val Asn Thr Pro Phe Gly
 530 535 540
 CAA TTC GCG CAC GCG GGC CTC CTC AAG AAT GAG GAG ATC CTC TGC CTC 2039
 Gln Phe Ala His Ala Gly Leu Leu Lys Asn Glu Glu Ile Leu Cys Leu
 545 550 555
 GCC GAC GAC CTG GCC ACC CGT CTC ACA GGT GTC TAC CCC GCC ACT GAC 2087
 Ala Asp Asp Leu Ala Thr Arg Leu Thr Gly Val Tyr Pro Ala Thr Asp
 560 565 570
 AAC TTC GCG GCC GCC GTT TCT GCC TTC GCC GCG AAC ATG CTG TCC TCC 2135
 Asn Phe Ala Ala Ala Val Ser Ala Phe Ala Ala Asn Met Leu Ser Ser
 575 580 585 590
 GTG CTG AAG TCG GAG GCA ACG TCC TCC ATC ATC AAG TCC GTT GGC GAG 2183
 Val Leu Lys Ser Glu Ala Thr Ser Ser Ile Ile Lys Ser Val Gly Glu
 595 600 605

ACT GCC GTC GGC GCG GCT CAG TCC GGC CTC GCG AAG CTA CCC GGA CTG	2231
Thr Ala Val Gly Ala Ala Gln Ser Gly Leu Ala Lys Leu Pro Gly Leu	
610 615 620	
CTA ATG AGT GTA CCA GGG AAG ATT GCC GCG CGT GTC CGC GCG CGC CGA	2279
Leu Met Ser Val Pro Gly Lys Ile Ala Ala Arg Val Arg Ala Arg Arg	
625 630 635	
GCG CGC CGC CGC GCC GCT CGT GCC AAT TAGTTTGCTC GCTCCTGTTT	2326
Ala Arg Arg Arg Ala Ala Arg Ala Asn	
640 645	
CGCCGTTTCG TAAAACGGCG TGGTCCCGCA CATTACGCGT ACCCTAAAGA CTCTGGTGAG	2386
TCCCCGTCGT TACACGACGG GTCTGCCGCG GTTCGATTCC ATTCCCAAGC GGCAAGAAGG	2446
ACGTAGTTAG CTCTGCGTCC CTCGGGATAC CA	2478

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Cf

Met Gly Asp Ala Gly Val Ala Ser Gln Arg Pro His Asn Arg Arg Gly	1 5 10 15
Thr Arg Asn Val Arg Val Ser Ala Asn Thr Val Thr Val Asn Gly Arg	20 25 30
Arg Asn Gln Arg Arg Arg Thr Gly Arg Gln Val Ser Pro Pro Asp Asn	35 40 45
Phe Thr Ala Ala Ala Gln Asp Leu Ala Gln Ser Leu Asp Ala Asn Thr	50 55 60
Val Thr Phe Pro Ala Asn Ile Ser Ser Met Pro Glu Phe Arg Asn Trp	65 70 75 80
Ala Lys Gly Lys Ile Asp Leu Asp Ser Asp Ser Ile Gly Trp Tyr Phe	85 90 95
Lys Tyr Leu Asp Pro Ala Gly Ala Thr Glu Ser Ala Arg Ala Val Gly	100 105 110
Glu Tyr Ser Lys Ile Pro Asp Gly Leu Val Lys Phe Ser Val Asp Ala	115 120 125
Glu Ile Arg Glu Ile Tyr Asn Glu Glu Cys Pro Val Val Thr Asp Val	130 135 140
Ser Val Pro Leu Asp Gly Arg Gln Trp Ser Leu Ser Ile Phe Ser Phe	145 150 155 160
Pro Met Phe Arg Thr Ala Tyr Val Ala Val Ala Asn Val Glu Asn Lys	165 170 175
Glu Met Ser Leu Asp Val Val Asn Asp Leu Ile Glu Trp Leu Asn Asn	180 185 190
Leu Ala Asp Trp Arg Tyr Val Val Asp Ser Glu Gln Trp Ile Asn Phe	195 200 205
Thr Asn Asp Thr Thr Tyr Tyr Val Arg Ile Arg Val Leu Arg Pro Thr	210 215 220
Tyr Asp Val Pro Asp Pro Thr Glu Gly Leu Val Arg Thr Val Ser Asp	225 230 235 240
Tyr Arg Leu Thr Tyr Lys Ala Ile Thr Cys Glu Ala Asn Met Pro Thr	245 250 255
Leu Val Asp Gln Gly Phe Trp Ile Gly Gly Gln Tyr Ala Leu Thr Pro	260 265 270
Thr Ser Leu Pro Gln Tyr Asp Val Ser Glu Ala Tyr Ala Leu His Thr	275 280 285

Leu Thr Phe Ala Arg Pro Ser Ser Ala Ala Ala Leu Ala Phe Val Trp
 290 295 300
 Ala Gly Leu Pro Gln Gly Gly Thr Ala Pro Ala Gly Thr Pro Ala Trp
 305 310 315 320
 Glu Gln Ala Ser Ser Gly Gly Tyr Leu Thr Trp Arg His Asn Gly Thr
 325 330 335
 Thr Phe Pro Ala Gly Ser Val Ser Tyr Val Leu Pro Glu Gly Phe Ala
 340 345 350
 Leu Glu Arg Tyr Asp Pro Asn Asp Gly Ser Trp Thr Asp Phe Ala Ser
 355 360 365
 Ala Gly Asp Thr Val Thr Phe Arg Gln Val Ala Val Asp Glu Val Val
 370 375 380
 Val Thr Asn Asn Pro Ala Gly Gly Gly Ser Ala Pro Thr Phe Thr Val
 385 390 395 400
 Arg Val Pro Pro Ser Asn Ala Tyr Thr Asn Thr Val Phe Arg Asn Thr
 405 410 415
 Leu Leu Glu Thr Arg Pro Ser Ser Arg Arg Leu Glu Leu Pro Met Pro
 420 425 430
 Pro Ala Asp Phe Gly Gln Thr Val Ala Asn Asn Pro Lys Ile Glu Gln
 435 440 445
 Ser Leu Leu Lys Glu Thr Leu Gly Cys Tyr Leu Val His Ser Lys Met
 450 455 460
 Arg Asn Pro Val Phe Gln Leu Thr Pro Ala Ser Ser Phe Gly Ala Val
 465 470 475 480
 Ser Phe Asn Asn Pro Gly Tyr Glu Arg Thr Arg Asp Leu Pro Asp Tyr
 485 490 495
 Thr Gly Ile Arg Asp Ser Phe Asp Gln Asn Met Ser Thr Ala Val Ala
 500 505 510
 His Phe Arg Ser Leu Ser His Ser Cys Ser Ile Val Thr Lys Thr Tyr
 515 520 525
 Gln Gly Trp Glu Gly Val Thr Asn Val Asn Thr Pro Phe Gly Gln Phe
 530 535 540
 Ala His Ala Gly Leu Leu Lys Asn Glu Glu Ile Leu Cys Leu Ala Asp
 545 550 555 560
 Asp Leu Ala Thr Arg Leu Thr Gly Val Tyr Pro Ala Thr Asp Asn Phe
 565 570 575
 Ala Ala Ala Val Ser Ala Phe Ala Ala Asn Met Leu Ser Ser Val Leu
 580 585 590
 Lys Ser Glu Ala Thr Ser Ser Ile Ile Lys Ser Val Gly Glu Thr Ala
 595 600 605
 Val Gly Ala Ala Gln Ser Gly Leu Ala Lys Leu Pro Gly Leu Leu Met
 610 615 620
 Ser Val Pro Gly Lys Ile Ala Ala Arg Val Arg Ala Arg Arg Ala Arg
 625 630 635 640
 Arg Arg Ala Ala Arg Ala Asn
 645

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 283..2307
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTTCCTTTCTTT	CTTTACCAAG	TGTGGTAAAA	TTTAAACAAA	GAAGAAAACC	AGGACCGTAA	60
CCCGGCCCTT	ACACACCTCG	AGTCCGTGAC	CACCGGATTA	TACGTCGCCC	ACCACACGGC	120
GCCTTTTCCG	ACCACTCTCG	AGAGTCGTTG	GGAGTTTCGT	CCGTGACCAC	CCGGTTGGCA	180
GTCGACAGAC	GCTTCCGGAC	CACTAGAACC	TCCTCGAGCG	ACGCACACAC	AGCACACACA	240
CCGCCTTAGC	TGCACCTACG	GCAGCGTTGA	TAGCGCGGAT	TT ATG AGC	GAG CAC	294
				Met. Ser	Glu His	
				1		
ACC ATC GCC	CAC TCC ATC	ACA TTA CCA	CCC GGT TAC	ACC CTT GCC	CTA	342
Thr Ile Ala	His Ser Ile	Thr Leu Pro	Pro Gly Tyr	Thr Leu Ala	Leu	
5	10		15		20	
ATA CCC CCT	GAA CCT GAA	GCA GGA TGG	GAG ATG CTG	GAG TGG CGT	CAC	390
Ile Pro Pro	Glu Pro Glu	Ala Gly Trp	Glu Met Leu	Glu Trp Arg	His	
	25		30		35	
AGC GAC CTC	ACA ACC GTC	GCG GAA CCC	GTA ACG TTC	GGG TCA GCG	CCA	438
Ser Asp Leu	Thr Thr Val	Ala Glu Pro	Val Thr Phe	Gly Ser Ala	Pro	
	40		45		50	
ACA CCG TCA	CCG TCA ATG	GTA GAA GAA	ACC AAC GGC	GTC GGA CCG	GAA	486
Thr Pro Ser	Pro Ser Met	Val Glu Glu	Thr Asn Gly	Val Gly Pro	Glu	
	55		60		65	
GGC AAG TTT	CTC CCC CTG	ACA ATT TCA	CCG CTG CTG	CAC AAG ACC	TCG	534
Gly Lys Phe	Leu Pro Leu	Thr Ile Ser	Pro Leu Leu	His Lys Thr	Ser	
	70		75		80	
CGC AAA GCC	TTG ACG CCA	ACA CCG TCA	CTT TCC CCC	GCT AAC ATC	TCT	582
Arg Lys Ala	Leu Thr Pro	Thr Thr Pro	Ser Leu Ser	Pro Ala Asn	Ile Ser	
	85		90		95	
AGC ATG CCC	GAA TTC CGG	AAT TGG GCC	AAG GGA AAG	ATC GAC CTC	GAC	630
Ser Met Pro	Glu Phe Arg	Asn Trp Ala	Lys Gly Lys	Ile Asp Leu	Asp	
	105		110		115	
TCC GAT TCC	ATC GGC TGG	TAC TTC AAG	TAC CTT GAC	CCA GCG GGT	GCT	678
Ser Asp Ser	Ile Gly Trp	Tyr Phe Lys	Tyr Leu Asp	Pro Ala Gly	Ala	
	120		125		130	
ACA GAG TCT	GCG CGC GCC	GTC GGC GAG	TAC TCG AAG	ATC CCT GAC	GGC	726
Thr Glu Ser	Ala Arg Ala	Val Gly Glu	Tyr Ser Lys	Ile Pro Asp	Gly	
	135		140		145	
CTC GTC AAG	TTC TCC GTC	GAC GCA GAG	ATA AGA GAG	ATC TAT AAC	GAG	774
Leu Val Lys	Phe Ser Val	Asp Ala Glu	Ile Arg Glu	Ile Tyr Asn	Glu	
	150		155		160	
GAG TGC CCC	GTC GTC ACT	GAC GTG TCC	GTC CCC CTC	GAC GGC CGC	CAG	822
Glu Cys Pro	Val Val Thr	Asp Val Ser	Val Pro Leu	Asp Gly Arg	Gln	
	165		170		175	
TGG AGC CTC	TCG ATT TTC	TCC TTT CCG	ATG TTC AGA	ACC GCC TAC	GTC	870
Trp Ser Leu	Ser Ile Phe	Ser Phe Pro	Met Phe Arg	Thr Ala Tyr	Val	
	185		190		195	
GCC GTA GCG	AAC GTC GAG	AAC AAG GAG	ATG TCG CTC	GAC GTT GTC	AAC	918
Ala Val Ala	Asn Val Glu	Asn Lys Glu	Met Ser Leu	Asp Val Val	Asn	
	200		205		210	
GAC CTC ATC	GAG TGG CTC	AAC AAT CTC	GCC GAC TGG	CGT TAT GTC	GTT	966
Asp Leu Ile	Glu Trp Leu	Asn Asn Leu	Ala Asp Trp	Arg Tyr Val	Val	
	215		220		225	
GAC TCT GAA	CAG TGG ATT	AAC TTC ACC	AAT GAC ACC	ACG TAC TAC	GTC	1014
Asp Ser Glu	Gln Trp Ile	Asn Phe Thr	Asn Asp Thr	Thr Thr Tyr	Val	
	230		235		240	
CGC ATC CGC	GTT CTA CGT	CCA ACC TAC	GAC GTT CCA	GAC CCC ACA	GAG	1062
Arg Ile Arg	Val Leu Arg	Pro Thr Tyr	Asp Val Pro	Asp Pro Thr	Glu	

245 250 255 260
GGC CTT GTT CGC ACA GTC TCA GAC TAC CGC CTC ACT TAT AAG GCG ATA 1110
Gly Leu Val Arg Thr Val Ser Asp Tyr Arg Leu Thr Tyr Lys Ala Ile
265 270 275
ACA TGT GAA GCC AAC ATG CCA ACA CTC GTC GAC CAA GGC TTT TGG ATC 1158
Thr Cys Glu Ala Asn Met Pro Thr Leu Val Asp Gln Gly Phe Trp Ile
280 285 290
GGC GGC CAG TAC GCT CTC ACC CCG ACT AGC CTA CCG CAG TAC GAC GTC 1206
Gly Gly Gln Tyr Ala Leu Thr Pro Thr Ser Leu Pro Gln Tyr Asp Val
295 300 305
AGC GAG GCC TAC GCT CTG CAC ACT TTG ACC TTC GCC AGA CCA TCC AGC 1254
Ser Glu Ala Tyr Ala Leu His Thr Leu Thr Phe Ala Arg Pro Ser Ser
310 315 320
GCC GCT GCA CTC GCG TTT GTG TGG GCA GGT TTG CCA CAG GGT GGC ACT 1302
Ala Ala Ala Leu Ala Phe Val Trp Ala Gly Leu Pro Gln Gly Gly Thr
325 330 335 340
GCG CCT GCA GGC ACT CCA GCC TGG GAG CAG GCA TCC TCG GGT GGC TAC 1350
Ala Pro Ala Gly Thr Pro Ala Trp Glu Gln Ala Ser Ser Gly Gly Tyr
345 350 355
CTC ACC TGG CGC CAC AAC GGT ACT ACT TTC CCA GCT GGC TCC GTT AGC 1398
Leu Thr Trp Arg His Asn Gly Thr Thr Phe Pro Ala Gly Ser Val Ser
360 365 370
TAC GTT CTC CCT GAG GGT TTC GCC CTT GAG CGC TAC GAC CCG AAC GAC 1446
Tyr Val Leu Pro Glu Gly Phe Ala Leu Glu Arg Tyr Asp Pro Asn Asp
375 380 385
GGC TCT TGG ACC GAC TTC GCT TCC GCA GGA GAC ACC GTC ACT TTC CGG 1494
Gly Ser Trp Thr Asp Phe Ala Ser Ala Gly Asp Thr Val Thr Phe Arg
390 395 400
CAG GTC GCC GTC GAC GAG GTC GTT GTG ACC AAC AAC CCC GCC GGC GGC 1542
Gln Val Ala Val Asp Glu Val Val Val Thr Asn Asn Pro Ala Gly Gly
405 410 415 420
GGC AGC GCC CCC ACC TTC ACC GTG AGA GTG CCC CCT TCA AAC GCT TAC 1590
Gly Ser Ala Pro Thr Phe Thr Val Arg Val Pro Pro Ser Asn Ala Tyr
425 430 435
ACC AAC ACC GTG TTT AGG AAC ACG CTC TTA GAG ACT CGA CCC TCC TCT 1638
Thr Asn Thr Val Phe Arg Asn Thr Leu Leu Glu Thr Arg Pro Ser Ser
440 445 450
CGT AGG CTC GAA CTC CCT ATG CCA CCT GCT GAC TTT GGA CAG ACG GTC 1686
Arg Arg Leu Glu Leu Pro Met Pro Pro Ala Asp Phe Gly Gln Thr Val
455 460 465
GCC AAC AAC CCG AAG ATC GAG CAG TCG CTT CTT AAA GAA ACA CTT GGC 1734
Ala Asn Asn Pro Lys Ile Glu Gln Ser Leu Leu Lys Glu Thr Leu Gly
470 475 480
TGC TAT TTG GTC CAC TCC AAA ATG CGA AAC CCC GTT TTC CAG CTC ACG 1782
Cys Tyr Leu Val His Ser Lys Met Arg Asn Pro Val Phe Gln Leu Thr
485 490 495 500
CCA GCC AGC TCC TTT GGC GCC GTT TCC TTC AAC AAT CCG GGT TAT GAG 1830
Pro Ala Ser Ser Phe Gly Ala Val Ser Phe Asn Asn Pro Gly Tyr Glu
505 510 515
CGC ACA CGC GAC CTC CCG GAC TAC ACT GGC ATC CGT GAC TCA TTC GAC 1878
Arg Thr Arg Asp Leu Pro Asp Tyr Thr Gly Ile Arg Asp Ser Phe Asp
520 525 530
CAG AAC ATG TCC ACC GCT GTG GCC CAC TTC CGC TCA CTC TCC CAC TCC 1926
Gln Asn Met Ser Thr Ala Val Ala His Phe Arg Ser Leu Ser His Ser
535 540 545
TGC AGT ATC GTC ACT AAG ACC TAC CAG GGT TGG GAA GGC GTC ACG AAC 1974
Cys Ser Ile Val Thr Lys Thr Tyr Gln Gly Trp Glu Gly Val Thr Asn

550 555 560
 GTC AAC ACG CCT TTC GGC CAA TTC GCG CAC GCG CTC CTC AAG AAT 2022
 Val Asn Thr Pro Phe Gly Gln Phe Ala His Ala Gly Leu Leu Lys Asn
 565 570 575 580
 GAG GAG ATC CTC TGC CTC GCC GAC GAC CTG GCC ACC CGT CTC ACA GGT 2070
 Glu Glu Ile Leu Cys Leu Ala Asp Asp Leu Ala Thr Arg Leu Thr Gly
 585 590 595
 GTC TAC CCC GCC ACT GAC AAC TTC GCG GCC GCC GTT TCT GCC TTC GCC 2118
 Val Tyr Pro Ala Thr Asp Asn Phe Ala Ala Ala Val Ser Ala Phe Ala
 600 605 610
 GCG AAC ATG CTG TCC TCC GTG CTG AAG TCG GAG GCA ACG TCC TCC ATC 2166
 Ala Asn Met Leu Ser Ser Val Leu Lys Ser Glu Ala Thr Ser Ser Ile
 615 620 625
 ATC AAG TCC GTT GGC GAG ACT GCC GTC GGC GCG GCT CAG TCC GGC CTC 2214
 Ile Lys Ser Val Gly Glu Thr Ala Val Gly Ala Ala Gln Ser Gly Leu
 630 635 640
 GCG AAG CTA CCC GGA CTG CTA ATG AGT GTA CCA GGG AAG ATT GCC GCG 2262
 Ala Lys Leu Pro Gly Leu Leu Met Ser Val Pro Gly Lys Ile Ala Ala
 645 650 655 660
 CGT GTC CGC GCG CGC CGA GCG CGC CGC CGC GCT CGT GCC AAT 2307
 Arg Val Arg Ala Arg Arg Ala Arg Arg Arg Ala Ala Arg Ala Asn
 665 670 675
 TAGTTTGCTC GCTCCTGTTT CGCCGTTTCG TAAAACGGCG TGGTCCCGCA CATTACGCGT 2367
 ACCCTAAAGA CTCTGGTGAG TCCCCGTCGT TACACGACGG GTCTGCCGCG GTTCGATTCC 2427
 ATTCCCAAGC GGCAAGAAGG ACGTAGTTAG CTCTGCGTCC CTCGGGATAC CA 2479

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Ser Glu His Thr Ile Ala His Ser Ile Thr Leu Pro Pro Gly Tyr
 1 5 10 15
 Thr Leu Ala Leu Ile Pro Pro Glu Pro Glu Ala Gly Trp Glu Met Leu
 20 25 30
 Glu Trp Arg His Ser Asp Leu Thr Thr Val Ala Glu Pro Val Thr Phe
 35 40 45
 Gly Ser Ala Pro Thr Pro Ser Pro Ser Met Val Glu Glu Thr Asn Gly
 50 55 60
 Val Gly Pro Glu Gly Lys Phe Leu Pro Leu Thr Ile Ser Pro Leu Leu
 65 70 75 80
 His Lys Thr Ser Arg Lys Ala Leu Thr Pro Thr Pro Ser Leu Ser Pro
 85 90 95
 Ala Asn Ile Ser Ser Met Pro Glu Phe Arg Asn Trp Ala Lys Gly Lys
 100 105 110
 Ile Asp Leu Asp Ser Asp Ser Ile Gly Trp Tyr Phe Lys Tyr Leu Asp
 115 120 125
 Pro Ala Gly Ala Thr Glu Ser Ala Arg Ala Val Gly Glu Tyr Ser Lys
 130 135 140
 Ile Pro Asp Gly Leu Val Lys Phe Ser Val Asp Ala Glu Ile Arg Glu
 145 150 155 160
 Ile Tyr Asn Glu Glu Cys Pro Val Val Thr Asp Val Ser Val Pro Leu
 165 170 175
 Asp Gly Arg Gln Trp Ser Leu Ser Ile Phe Ser Phe Pro Met Phe Arg

180 185 190
 Thr Ala Tyr Val Ala Val Ala Asn Val Glu Asn Lys Glu Met Ser Leu
 195 200 205
 Asp Val Val Asn Asp Leu Ile Glu Trp Leu Asn Asn Leu Ala Asp Trp
 210 215 220
 Arg Tyr Val Val Asp Ser Glu Gln Trp Ile Asn Phe Thr Asn Asp Thr
 225 230 235 240
 Thr Tyr Tyr Val Arg Ile Arg Val Leu Arg Pro Thr Tyr Asp Val Pro
 245 250 255
 Asp Pro Thr Glu Gly Leu Val Arg Thr Val Ser Asp Tyr Arg Leu Thr
 260 265 270
 Tyr Lys Ala Ile Thr Cys Glu Ala Asn Met Pro Thr Leu Val Asp Gln
 275 280 285
 Gly Phe Trp Ile Gly Gly Gln Tyr Ala Leu Thr Pro Thr Ser Leu Pro
 290 295 300
 Gln Tyr Asp Val Ser Glu Ala Tyr Ala Leu His Thr Leu Thr Phe Ala
 305 310 315 320
 Arg Pro Ser Ser Ala Ala Ala Leu Ala Phe Val Trp Ala Gly Leu Pro
 325 330 335
 Gln Gly Gly Thr Ala Pro Ala Gly Thr Pro Ala Trp Glu Gln Ala Ser
 340 345 350
 Ser Gly Gly Tyr Leu Thr Trp Arg His Asn Gly Thr Thr Phe Pro Ala
 355 360 365
 Gly Ser Val Ser Tyr Val Leu Pro Glu Gly Phe Ala Leu Glu Arg Tyr
 370 375 380
 Asp Pro Asn Asp Gly Ser Trp Thr Asp Phe Ala Ser Ala Gly Asp Thr
 385 390 395 400
 Val Thr Phe Arg Gln Val Ala Val Asp Glu Val Val Val Thr Asn Asn
 405 410 415
 Pro Ala Gly Gly Gly Ser Ala Pro Thr Phe Thr Val Arg Val Pro Pro
 420 425 430
 Ser Asn Ala Tyr Thr Asn Thr Val Phe Arg Asn Thr Leu Leu Glu Thr
 435 440 445
 Arg Pro Ser Ser Arg Arg Leu Glu Leu Pro Met Pro Pro Ala Asp Phe
 450 455 460
 Gly Gln Thr Val Ala Asn Asn Pro Lys Ile Glu Gln Ser Leu Leu Lys
 465 470 475 480
 Glu Thr Leu Gly Cys Tyr Leu Val His Ser Lys Met Arg Asn Pro Val
 485 490 495
 Phe Gln Leu Thr Pro Ala Ser Ser Phe Gly Ala Val Ser Phe Asn Asn
 500 505 510
 Pro Gly Tyr Glu Arg Thr Arg Asp Leu Pro Asp Tyr Thr Gly Ile Arg
 515 520 525
 Asp Ser Phe Asp Gln Asn Met Ser Thr Ala Val Ala His Phe Arg Ser
 530 535 540
 Leu Ser His Ser Cys Ser Ile Val Thr Lys Thr Tyr Gln Gly Trp Glu
 545 550 555 560
 Gly Val Thr Asn Val Asn Thr Pro Phe Gly Gln Phe Ala His Ala Gly
 565 570 575
 Leu Leu Lys Asn Glu Glu Ile Leu Cys Leu Ala Asp Asp Leu Ala Thr
 580 585 590
 Arg Leu Thr Gly Val Tyr Pro Ala Thr Asp Asn Phe Ala Ala Ala Val
 595 600 605
 Ser Ala Phe Ala Ala Asn Met Leu Ser Ser Val Leu Lys Ser Glu Ala
 610 615 620
 Thr Ser Ser Ile Ile Lys Ser Val Gly Glu Thr Ala Val Gly Ala Ala
 625 630 635 640

Gln Ser Gly Leu Ala Lys Leu Pro Gly Leu Leu Met Ser Val Pro Gly
645 650 655
Lys Ile Ala Ala Arg Val Arg Ala Arg Arg Ala Arg Arg Arg Ala Ala
660 665 670
Arg Ala Asn
675

C4 (2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGGGATCCAC AGTTCTGCCT CCCCCGGACG GTAAATATAG GGGAACCATG GTCTAGAGG 59
